

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC
 TGCAGACTAAACCAAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTATTTTC
 TGGATCACTGGCGTTATCCTTCTTGAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCTTCGTGCTCATTGCTACTGGTACCG
 TCATTATTCTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
 AAACGTGATGCAATGTTTCTGACTCTCGTTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
 ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
 TGTTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
 TCCTAAGAGTTGCTGTAAACTTGAAGATTGTA

10
 9
 8
 7
 6
 5
 4
 3
 2
 1

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSVLENYFSLLEKATNVFF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

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FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCCTCGCGTCCATCTTTGCCGTTCTCTCGGACGTGTACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCCGACCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAAGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
 GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGTTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAGTTGTTAAAAACAAATAGGATGCAAATTCC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACCTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAAATCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTTGCGCCACCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAAACAAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEIHAFGLTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPFRGRGPHEPRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC
 CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCTAACGGAATG
 CAAGATGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
 CAGGTGCCTGGGCGATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
 CTTCCCCGACATAACCTTCGGACTAGTGCAGAGCAAACCTTTCCCTTCTACTTCCACATCTC
 CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
 CATTCCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAAC
 GCCCCTGGCTGGAACCCCGACCAAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
 GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
 GAGAGAAGGACCCCAAGTACAGTGTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
 TCTCTTTGCAATCTGGGCTGCGTCTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
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 AAAAAAAAAA

101536.121201
 101536.121201

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGNLLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFFPYFHISM
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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCLNLCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

1035786.12101

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTTTCATGAAC TAGCAAGAGGACACCATCTT
 CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
 AGAATCTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCA
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAAGGATTGTCAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGAAAAGATGCCAAAATTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGTGGTGGTATCCCAGGGTCCCTG
 CTAAGTTTTCTTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAATGAAAGACTTGCCCATTCAAAATG
 ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT
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FIGURE 8

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><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYEGGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCC**ATGG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTTGACGCCGCCAGTGGCGGGGGCCCCCTTGGGCCGTGCGCCACCCT
 GTAGTCATGTACCCACCGCCGCCGCCGCCGCTCATCGGGACTTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATTGACAACAGCAAGAGTTGGCGCGGGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTGCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTCTGT
 GGACTCCTCTTCTACATCACTTGGCTGACCATTGGAAGGCTCTGGCTTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAACCAGCAAATCCACCCGCTCTTACCAG
 CTCCTCAGAAGGCCGACACCGACCCTGAGAACTACCTGAGATTTTCGTACAGAAGACACAA
 AGACACATCCAGCGGGGACCACTCACCTGCAGATTAGACCCCCAAGCCAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAGCCCTGTGGATCCCCGCCCGGAAGGAG
 ATCCGCAGAGGACAGTATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGTCTTCTGCATGCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTTGAAAAGGACG
 TGGACGTCAACTGTTTGAGAGCACGATCCGCATCTGGGGGGGCTCCTGTGTCCTACCAC
 CTGTCTGGGGACAGCCTTCTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCTTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCCGTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACACAGCATCAGCTGGAGTTCCGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAAGTTTCAGGAGGCAAGTGGAAGGTTGACACAGCA
 CATCCAGCGCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
 AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACCTCCGAGCCCAAGTAAAGCTCACCTTTG
 TGGGGGAGCTTGGCCAGGGCGCTTCAGTGCCAGATGGACCACCTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCGCCAGCCATGGAGCTGGGCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCATTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTCTACCTGTACC CGCTCACAGGGGA
 CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACCGGGTCC
 CCTCGGTTGGCTATTCTTCCATCAACAATGTCCAGGATCTCAGAAGCCCGAGCTTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGTCTTCTCCGATGA
 CCCAAACCTGCTCAGCTTGACGCTACGTGTTCAACACCGAAGCCACCCCTCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTGACCCGGCAACGCCAAGTGGGCCAGGCT
 CTGAACCTGGCTCTGGGCTCTCTCTGCTCTGCTTTAATCAGGACACCGTGAAGGCAAGTGA
 GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTCTCTCT
 CAGAAGACACGAATCATGACTCAGGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACA
 GAGGGGGGCTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGACG
 TCTGCCCGGGCTCGTAAGCCTCAGATGCCCAATCCAAGGCTTGGAGGGGCTGCCGTGA
 CTCAGAGGCTGAGGCTCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC
 CTGGCCGCCCGCAGGGGGCTGGAGGGCTGGACGGCAAGTCCGCTCTAGCTCAGGGGCCCT
 CCAGTGGAAATGGGCTTTTCGGTGGAGATAAAAGTGATTGCTCTAAGCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

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 IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTOEEAT
 KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTPVHLNY
 RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLTLIDALDTMWILGLRKEFEEA
 RKWVSKKLHFEKDVVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
 PYSVDNIGTGVAHPPRWTSDSTVAEVTISIQLFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
 KDGLVPMFINTHSGFLTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
 HLLRHSEPSKLTFFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
 MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRPETVESLFYLYRVTGDRKYQDWG
 WEILQSFSRFRTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
 AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
CGCCTCTCCGCACGATGTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGACGGC
AGGTCGGGTTGCTCTCCGGCGGCCTCCCTCGAAAGTGTTCCGCTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCTGGCAGTGCTGGT
GCCCTTCCGGAACGCTTCGAGGAGCTCTGGTCTTCGTGCCCCACATGCGCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCCTGTGCTCTCCAAGCAGCACTACCGGCTGTGAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCCGCAGGACGACGAGTTCTACCGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCTCGGGAATCACAAC TGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGG
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCCGCACACCTGGTGCACATTC
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
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FIGURE 12

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><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSSRRKAAQLPWEDGRSGLSGGLPRKCSVFHLFVACLSLGLFSLLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFPVPMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFELESSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGCT**TAAG**AAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTTATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

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PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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102121" 99255001

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
GAGCATGTCCGCGCCGGGGAGGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
GCCCGCCCGCGCTCTTCCCGCCCGGGCTCCGGGGCGGCCGCTAGGCCAGTGCGCCGCCG
TCCGCCCGCAGCCCTCCGGCCCGCAGCA**ATGG**AGGCCACCCGAGCCGCGGGCGGCCGCGCA
GCCGCCGTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG
GCGGCGCGCCCGCGCGCTGCCCGCCGGTGC AAGCAGATGGCGGCCCGCGAGGGGCTGGC
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GCCCCCAGATACTCTGCCCAACCGCACGCTCACCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACC AATCTGGTTC
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TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAAACATACTGTGGAT
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GAATTTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGACAGACCT
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GAGCTCACGTTTATTTCAACATATTACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
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ACTTTTCGGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
GCAATGTTTTCAAATACATTTTCGAGTCTGGCACTAAGGTTATTGTACATTTCTGCAATCTTT
AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAATGTTCTGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTTCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACTA
ACCGGAAGAAGCTGCATTACACTTTCAGGGCCCTAGGCATTTTTTGCTTTGATTCCCTTT
CTTCACATAAAAAATCAGAAATTACATTTTATAACTGCAGTGGTATAAATCAAATATACT
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GATTTTAAAGCAATAAGATGTTTTTCATGGGCCCTAAAAAGTATCATGAGCCCTTTGGCACTGC
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ATCAAAATTTTGGCAGAAAAACAATAATGTCATATATTCTGCTGCGGTTTTTAATCTCACAG
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TGCATAATAACTGATCCCAACAGGTGTTAGGTGTTCTGCTTTAGTGTGAGCACTCAATAATA
TTGAATGAATGAACGAAAAAAAAAAAAAAAA

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FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSELELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSSLKRDLDTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPELPSFYMTF
 SHRQVVFEGDSLPPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVNNKGDFRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMLNL
 TNAVATARQLLAYTVEANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

GCGTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGTCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
 ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
 CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
 TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAA
 TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
 GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
 AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTTCAGGGTCCCTTATATCTGAATAAAGGA
 GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
 TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
 TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
 TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

10121" 9255001
 00536 12301

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

10015386.121201

FIGURE 19

CTGTCGTCTTTGCTTCAGCCGCACTGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCC
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAAACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTTACCTGGTGTCTTCTGCTTCTCCGTGACCCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGGCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTCTGTCCACGCGCGTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCTTGAGCCCGGGCCCGGCCGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTGCGCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGCCATCGCCATCTGTGTAACCTGGGG
 GAGTGCACCAAGTGTACCCATCCCCTTCCCAGCTTCTGTGCGGGCTGGCCTTGTGTGTC
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCTCTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACTCTGCCCACTGGTTTTGTCAAGGTCTTAAGACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTCTTGTCTTCTTGCCGAGTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTCTCCTGTGTTTTCTCTTCTGCTCTCCCTCCCTCCACCTTTTCTTTCTTCC
 CAATTCCTTGCACTCTAACAGTTCTTGGATGCATCTTCTTCTTCCCTTTCCTCTGTGT
 TTCCTTCTGTGTGTTTTGTGTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTCAAGCGATTCTCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCTGTGCGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGCTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCGCTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAAAAACATATATATATAT
 ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAACACCGACCCTGGGTCCCCTAGG
 CCCCCTGCGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGTGGATGCCTTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

1001336-121301

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLASASIIYPTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPAAEWCAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFEKV
```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

TGAAGCTGCCACATGCCCTATTAATTTTGAATTTTGTAGTAGAGACGGGGTTTCCACATGTTGGCCAGGCTGTGCT
 TTAAGCTGTGACCTCATGATCCCTCACTCGGCTCCCAAGTGTGGTATACAGCATAGGACCATGACCTGCT
 CTGGCCAGCCTCATGATTTTAAAGAAATTATCTGTATTAGTGTCTCTGTAACAACTTGGGCATACAGTGACCA
 AAGACAGCTGAATTTCCCCAAGGACCAAGACAGGTGAGGAGACACACAGAAACAGGAATGCAAAAGAGACCA
 TTTATTACTCACTATGACTAAGGGTCACAAATGGGTACGTTGATGGAGAGTGATTTTAAAGACATCAGAGG
 AGGACAGACATACCAAGAGAGGCGCCAGGAAGCTCTCTGACAGAGGTGGTATTTGACGCCAACTGGGAAGAATG
 GAAAGAGCTAGCCAGGCATCAGATAGTCCAGAAGAGTGGGAGAGCATACACTACATCACTATTGGCCTAGAA
 AATAGCACTGGGATTTGAGGAGAGCTGGGGGACACAGGTTCTGCCCACTGGGACAGGAGCAATGAGGGCTTGA
 AAGGGCAATGCGAGTAGAGTAGAAGAAAGGCTAGGAGAGGAGCACTTTCAGGTGGGAATTAATAGGTTCTTA
 AACGATATAGGCAAGCAAGGACAGGGGAGAAATGTATGGTAAATGCTGAGTTTGAGCGAGGCTAGATGGGACAG
 TGSTGGGTGATGCAAGGAAGAAAGCTCAGGAAGAGCCGACAGCTGGGGAAGAGTGTGGGCTTTGGTTTCCA
 TCTTCCGAGTGTCCGGAATGTGGATGGGAAGACACAGAGGAGGACAGAGGAGGAGAGGGAAGGAAATCTAA
 AGAAGTCTCGAGTGCACACTCTTCTTCT
 TTTCTGCCCTGCTCTCACTCTCTCTGGGTGCTGGGAAGTGGAGATAGCTGAAGTTTGTCTCTCGGGGCTGT
 TCGAATTCCTCAATGTTCTTGGGAGACATAATCACTGTCTCTAGCTTTCTATFACATTTACATTTCTCTGTAG
 CACTGGGACATATGTGTGGTGTCTTCTTCTAGCT
 GCGGAAAGTGTACTGCTGTAGAGGCTGACTGACTTTTAATGGTGTATCCAGAGTGAAATGTGGAGACAGTGT
 CGGATGCTGTGCCAAGTCCGCGGACGCCCTAACTATCCAGGAAGTCCGCTGCGCTGGCAGAGTCTCCCTGATGT
 ATGACGCCCTCTCAGTGTCTTGTGCGCACTTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GTGATGATCATGTGGGTGTCCCTTCTTCT
 ACATGGATCTTAACCTATGCAACCTTCCACCTCTGCACTGCACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 TCCACCTTCCCTATCTCAGGATTTTCCAGGTGGTGAAGGACAGCTGACCAACGCTCAAGCAATGGCCACAGG
 CGCGAGTGGCTCACTTCAATGATGGGAAGGCTGAGACAGGCGAGTCACTCACTGTCTCTCTCTCTCTCTCTCT
 TTTCT
 TCGCGAAGCCATGCTCCAGATGGTCTTCGTGTGATGGGACGACTCACTGATCTCTATGATGAGCACT
 TCTGTGGGGAATGACACAGATGGCTGTGGGACGCTGCCCTGGGCGCGACCTCTCAGGACCTGTCTACGGGCC
 ACCGTTCTCCCGGCTCTGCGCGACGGTCTGCTGGAGCTCTGAGCGAGCTCTCAGACAGCTGTCTCCGACAGCA
 CGCTGTGCTTGTGTGTGTCAGGCTGGAGTGGGTGGTGGGCTCCCGGCGGCTGCGCTCCGAGCTCGTGG
 GCGATGACTCTTCTCGCAAACTCGCCCGACGGGAAAGTGTCTCTCGAGCTCTGGGCGCTCTGGGCGCTCT
 AGGACTCACTCTACAACCTCTCACAGAGTCTGCGAATTTCCCGCGGAGGAGGAGCGGCCCTCTCAGGAG
 ATCGTCAGCCTCATCGCCACCAATACAGGCACTGGGAACGCGAGCGCAAGCTCTGACTCGGCTCTCTCTCT
 GSGTGTGTCTTAGTAGAGGATGAGGACAGCAGAGAAGCACTGACCCCACTGCTGCGTGGAGTGGATGCA
 TCCCGCGCTGTGCGAGGGCAGAGCTCTGTGTGCTGTGGCTCAAGGCTCCAGCAGACCTCCACAGC
 TAGAGCGCTCTGGGAGGCTCGCTCTCTGTTGGTATTTGCAATGAAGTGTGGAGAGGAGGCGGGGCTGT
 GCGTGGGCGGCGATGTCTGCCCCACTCCGGGGCTTGGCGGGGTTGCCCGGGGCTCTGGGCAATGGCTACA
 CGTGTGGACAGCATGTATGTTCTATGTTTAAATGCCACACACAACTTCTCTCGGATAATGAACACTA
 AGGGGGTGTGACTGGGTGTGGAGGTTGGGTGGGAGGGGCGCCAGACCCCACTCCGATCCCTGCTCTCT
 TGTCTCTGCTTTTCTCTCACTTCCGAGTCAATGTCAGTGTGTAGATAATACCCCACTCGAGGGCGTGG
 CTCTCGGCCCTCGGAGCTATGAGTGTGAGCTGCTCTCAAGGGCCCTCGGCAGTGGGCTGTGTTGTGCTCT
 ATCTCACTTCTCATGTCTCTAAATTTCTCTCTTTTCTCTTAAAGACAGAAGTTTGTCTGTTTCTAGTCT
 GGATCTCTCTTCTCTGGGAGGCTTGGATGATGAAGACATGACCTTCAACCTTTCTGGGCCCTCAATGG
 GCGCTGGGCGCTTCCCAACCTCTCATGAGTGTGCGGCACTGTCTGGCGCTCTCACAGCGCGGGCTGCC
 ATTCCAGCAGAGCTCTCTGAGCGGAGGTGGGAAGAAAGTGGCTCTGTGTGCCACAGCTGGGAATCTATGTT
 CTCTAGAGAGGGCCACAGAGGCGCCAGGGGTGCGCGGAATGTGACGTGATGCTGCTGAGAGGACGGAAT
 TGTGCCATGAGTGACAGTCATGAGGAGGTGTCCTCTCTGGGAGGGAAGAGGTAGAGCTTCTGTCTGAAT
 GAAAGGCGCAAGGCTACAGTAGAGGCGCCGCGCCAGGCACTGTTAATGCCCACTGTGAGGCGCTCGGAC
 ATCTTGCAATCCCAAGTCACTGAGCTAGCTTTTATGTTTGTGGGAGAGGTGGGTGGCTTTAGAAATTAAGGC
 CTGTAGGCTTTGGCAGTGAAGGCGCCAAAGTAAAGACAGAGAGCAAGGGCAGGATCTATATATAGT
 GCGTCATTAGGTGTTATTTGTCTATTAAAGATTTGTTTATTAATTAATATAAAATCTTGTGAATCTC

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSLAQVNLSPFSSHVKVHMDPNYCHPSTSLHLCS
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAAGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSLCSLEDGLGSPARLASQLLGDE
 LLLAKLPRESAFRSLGLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCTCTGGGCGCTCTGTTACACAAGCATACAGCCAGCCCCACCTAATTTTGTTTCCCT
GGCACCCTCCTGCTCAGTGCACATTGTACACCTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCTTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTCTTCACTCTGAAAAATGGGCATAA
TACAATCTATTCTTGGCCACATCAAGGGATTGTTATTCCCTTTAAAAAAAACCAATACCAAAG
AAGCCTACATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAAACACAGAACATTGCAGAAGTTT
TTAAAAAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGCTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAATTCAAACCTCTTCCAA
ATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGAAAAAGGAAAAC
GGATTCAATTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
ATGACCCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT
GATTGAGCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTACTTCTGTATTAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
CATCTAGCCTTTTGACAAATTTCATCTTTCAAAGGTTACACAAAATTACTGTGACGTGGAT
TTTGTCAAGGAGATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTTTGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTCTTAGTAGAAAAATATTGTGGAATCAGATAAACTAAAAGATT
TCACCATACAGCCCTGCCTCATACTAAATAATAAAAAATTATCCACCAAAAAATCTAAA
ACAAATGAAGATGACTCTTTACTGCTCTGCTCGCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
CTTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGCTCTTAATATATCTTAGGCTTCAA
TTATTGGGTGCCTTAAAACTCAATGAGAATCATGGT

1005336.124201

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHFSVSKVPWNA
PIADEDLLPISAHPNATPALSSNFVWTLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDTSFHRRLYDDRNEPVLRLDNAPEPYDVSVFGNSSYYPNTLNSA
MPSEENARDGIPMDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGACGCTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTACAAAGTACT
 TCATGCCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTTCGTGA
 GGATGACAACTTGCAATCATTGATGTGCCTGTCCCAGTTTCTCTGATAGTGACCCCTGĆAG
 CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAAGTGC
 TATCTGATGCCCCCTCAATACITCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCCCTTCGTCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**CT**
AAGAGGCAACAGATAGAGTGTCTTGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAACTACTAACCACTGCAAGCTCTTGTCAAATTTTAGTTTAAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTATAG
 GGTTAGATTTCTGAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
 GTTGTTTTTTTTGTTTGTTTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATTTGTTTTGAACTTTTTGTGTAAAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTGCAGTTCGTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAA
 CCCATAATAAATTTTACTCTATACAAAAA

10015366 "121201

FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDSPANLGRGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAIIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPKPNLVELFGKLASG
RLPQTYVVRDELVAEEIRDVSNLGIIFIYQLCNRKSFRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKIOAE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCAGAGCAGCCCCGGGCACCAAGCAGGACTCTCT
 CTTCCAGCCAGGTGCCCCCACTCTCGCTCCATTTCGGCGGGAGCACCAGTCTGTACGCC
 AAGGAACTGGTCTGGGGGCACCA**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCTTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCTTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAAACCTGGGG
 GGCCCATCCCCCACCACCTTCTGGATGGGATAGTGGACTTCTTCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGTCA
 TCACCCGGCAGAAGCAGAAGCCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCTCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAAGGGCAGCCAGGAGGGGGACAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGT
 AGGGGGCTGTGGTGGCCGGTGAAGGCCAAGGGGAGCTGGAAGGGTCTCTTTGTTAGCCAG
 GAAGCCCAAGGACCAAGTGGGTCCCCCGAAAGCCCTGTGCTTGACAGAGTGTCCACCCAG
 TGCT**TAAC**AGTCTCTCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGATCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACTCAGCAGCCCCAAAGGGCTACATCTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCAGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACACTTTTAAACA
 GCTACAGGGTAAATCTGCAGCACCCTCTGAAAATACTGCTCTTAATTTTCTGAAAG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCGGCCTGGGGGTGAGTTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCACAAATATTCTGCAGTCCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAAATAAACCTTTATTCCGGCTGAAAAA
 AAAGA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248



FIGURE 29

GTGGACTCTGAGAAGCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
GGGAGGACAGGGAGTTCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
GCAAGGAGGAGACCTTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATG
AAGTTCCAGGGGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
TGGGAGAGCCCTTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCT
GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
GATGCTGTCCGCGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGTCTGGGAAACTTCTGG
AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTGGGACCAACAC
TCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAAGTGGAGGCCAGCAACCAGAATGAAGGGT
GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCTCTCTGGGGA
TCCAGCACCGGCTCCTCCTCCGGCAACCAGGTGGGAGCGCGGAGGAAATGGACATAAACC
CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGAGCGGGGAATCTGGGATTAGGGCTTCA
GAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTGA
GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGTGACGCTGT
TGGTGGAGTCAATACTGTGAACCTGAGACGTCTCCTGGGATGTTAACTTTGACACTTTCT
GGAAGAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
AGCTCTCGCATCCCGTGACCCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACT
CCCTCCTTAAACACCAACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTA
GCTGCCCCACAA
AA

1015366.121201

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGQGGNGPPNFGTNTQGAVAQPGYGSVVRASNQNEGCTNPPPSGGSGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRL
GGSGDNYRGQSSSWGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

10015386.121201

FIGURE 31

GACCGGTCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGGTCTCACCG
 TGCCTTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCTTGTCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGAGGAGTGAAGGGAAATGTTTCTTGAAACAAGC
 TGTGCTACTTGTGCTCCTGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG
 GTCCTCATATTGCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGACAAATGCCCTGTGGTGGACACG
 AGCTGCTCTACACCTGCTGCCCTACATCGAGAGCTCCGGAACTGCTCCTTCTGGGGTGTGAGGACAGTGT
 GACGGAGTGGGGCTTCMTGAGGAAATCACCCACACTACCACAGCTGGGAGCCAGCTTCCACAGCCA
 GCCAGGGGCTGCAGGCACAGCTCCGCCAGGCTTTTCCACAAACAGCCGCCCTCTTGGCCGGACCGTAGAGT
 TCGTGGCAAAAGAAATTGATCAAACTGTCAAAATATCAAGGCTACACTGTTGGCAGATCTGGTGGCCAGS
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGAGACCCAGCCAGCTGTTGGAGATCT
 TGTCTTCCAGCTGTGCCCTCACGGGGCCACGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGGGGCGCTGCTTCCAGAGGAGACCCCGGACGGTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAAGCCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TTAGTGCACACTTTCGAGCCAGGGTCTGAACTGCTGCCGGGGGAGCGGAGGGGCTGCTCCGCGGCC**TGAC**
 GTGCTCTCCTTGGCCGTGGGGCCACGGGACCTGACGAGGGAGTCTCCCCAGAGCATCTGGAAACAGCTCCTAGGC
 CAGCTGGGCCAGAGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAAGTCTCTGTG
 GAGTTAGCTTCCCTCCTCTTGACAGTCAAAATCTCTATCTTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG
 CAGGCTGGAGAGCTTCTGCACATGCTGCTTTCTTGTGGAAGGAAGACTTTCAGGAGCCGCTTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTCTGGCAGACACAAGGCCAAGGAGTGGGACTTGTGCTATTCTTGCTA
 CGGGAGCTGGTGGAAGGGTCTGATGGGACGGATGGAGTAGAGGCTGCTGGGCAGCTTCCACAGGCCAG
 TGGCCAGGGGACTTGTCTGAAGAAATTAGCAACACTGTCTAATCTGTTTCTAGCCAGGCCACCTGCCAGAACCC
 CAGCTAAGAGCTGTGAGTTGGTGCGACCAAAACGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGCATTGCACAGAACCCCTGGACCCCGCTCACGAGGAGGCCAAGTGCCTAATGCAGACCTCAC
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAAGTCTCTGCTCTAAGGGTGTCACTGGCTGGCATCCCAACAGCGA
 ATCTAGAGGAAGGAGTGTGGCCTGATTTGGGATTATGGCAGAAAGTCCAGAGATGCCAGTCTCTGGATAGAA
 GAGTGGTGTGTGTTTATCTCTTGATATACTAAATGAAATGAGGTGTGGGGCTTGTCAACACAGAATCAAGCCT
 CATTTGCTATCCAGCATCTCTAAACTTTGAGTCTTGAATTCATGACAGAGGCAAAATGACTCTGCTTAAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGAGCTGGACTGCCATCTCCTT
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCTGTAACTCCAGCAGCTTTGAGAGGCTCAGGTCGGCG
 GACTGCTGAGGTGAGAAATCAAGACCAAGCTTGGCCAACTGGCAAAACCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGTTGCAGTAGCCGAGGTGCGACCACTGCACCTCCAGTCTGGGTAAACAGAGAGACTTTCTAG
 AAAAGCTTAACAAACAGATAAGGTAGGACTCAACCACTGAAACCTGACTTTCCCTCTGACTTCACTCCCTCT
 TGCAGCTATAAACCCTCTTGAGACTCTCCCTGACCAGGGACCAAGCACAGGCATTTAGAGCTTTTAGAATAA
 CTGGTTTCTTTTAAAAAATAAAAAAAGGGCGGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 TTTTCTTTTCTTTTAAAAAGGCTTTTATTAATACTCTCCCAAGAGTGGCTGCTGCAATCTGCCACAGCT
 TGGGGCGTGTCTCTAGGGAAGGCCCTGTTTTCCTGAGCGGGCTGGGCTTGTCCATGGTCCGCGGAGCTG
 CGCCTGTTGGCGCCTTGGCTGTCTACTGCTTCTGCGGGCACAGAGCTCGGGGTCTGGGGGACCGCGG
 AGCTAAGACAGAGCTCTGTTGCAGGCTGGAGGCTGTCTCTTAACGACACCTGAGTGTCTCTGAGATGCTG
 GGTCCACCTGAGTGCCAGGGAGCAGCTGTGGCCGCTGCTCTCTYTAGGCCAGTCTGGGGAACATAGCTC
 GGGCCCTTCTTTGCAAGAGGAGATGGGGTGGGTGGGGGACTCATGGGAAATGGGCTGAGGAATACGTGTG
 GAGAGGGCGCCGCTTGTGTGGCTGCAGCGGCTGGAGCGCTCTCTCTGAGCTAGTGTTCCTTTCCGCTCTA
 ATAGAAACATGCGCTGCGGTGCTCAGGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACGGCGCTCAT
 GTTATTTTCACACTGTCTCGGACGTTGGCTGGGACGCTCATGGAATGGCCCATGTCCCTCTGCTGGGTGGAC
 GTCGGGTGGGAGTGGCAGCGAGGGCGGGGCCAGAGCTGCGCTGGGGGTGAGGGAGGCGCCGGGAGGGG
 CCTCAGAGAAAGTGGGCTCCGCAACCAAGCAGGCGAGGCGGGCTCCCGCGCGCGCGCGCCACACCGCTCCAG
 GCGCGTAGCAAAAGTGCAGCTGCGCTTGGCTGCTGCGCAGAGGTAGCCCTTGATGCAGTGGGCGAGCGCG
 TCGTCCGCGAGCTGGAAGCAGCGCGCTCCACCAACAGAACAGCGGCTGCGCT

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FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPHEGLDNAPVVDQQLLYTC
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPQQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
 IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGGCCAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGAGAGAAATG
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGTCCAAACAGTGCCAATGAGGTCTTCCATTACGGCTCCTCGCGGGCCGTA
 GCCCGCAGCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCACTGTGTGATTGTGACAGCTCCAGCCACCTGCT
 GGGCACCAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGTGATGTGGGCAACAAGACCCTACCCGCTCGTGCGCCATTCC
 AGTGTGTTCGCGTGTGAGGAGGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTTCTGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCGCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGG
 CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGTTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCATG
 GCATGGTCCCCCAACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGCCGGACGAATGTGTCACTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGTTTCATACCAGAGAAAAGGGTCTTCTCATCGTGGGCCCATGTATGGCA
 TCACCTTCTCCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCA
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTGCCAAGGAGCTGGGAACCTGGTGTG
 CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGTGAAGCTGTCTGAGGCC
 GGCCAGAGAAATTGTGGGGTGTGAGAGTTGTGGGGCGGTGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGCTTGTGCTGTGCCCTGAGACCTTGGACAAAACCTTCCCCCTCTCTGGG
 CACCCTTCTGCCACACCACTTTCCAGTGCAGGCTGTGAGACCTTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACTTTAGGGTATTTTTGC
 GCAAACCTCTCAGGGTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTCCTTTTCTGCCCT
 CTAGCAGGGAGTTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGCTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT
 ATCACCTGGGTCTGTCCCCCTGGCTCTGTATCAGGCACCTTATTAAGCTGGGCCCTCAGTGG
 GGTGTGTTGTCTCTGCTCTTCTGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
 GGGCGTACTGCCACACTTGGTTTTTGTAAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAA

10015386.121201

FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLLGTLKGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFRVLRRPQEEFVNRTPTETVFIWGPSPSKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRRGETGKDREKSHSWLSTGWFTMVIARELCDHVVHVGMPVPPNYCSQRRLQRMPIH
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

10015336 121201
 101212 08551001

FIGURE 35

GTTTCCTCATATGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGAGCTT
 GAGGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGGTGTCTGAGGGGCTGG
 GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTTGGAACCCATGACCCATGAAGTCTTGTGCACATTTATACCGT
 CTGAGGGTGGACAGCTCGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC
 GGCTATGGGACGTTGGCTTCAGACCTTTGTGATACACATGCTCGGTGGGACGATCAGCGCGTGGAGAGGAATG
 AGGCTCTAGGTTACACTGGCTTGCCCTCTCTAGCCACAGCAGGCTGCTTGTCTGACTTGAACGAGGTCCTCTAG
 GTCCAGCTCCAGCTCGCTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGGTGGTGGAACTCCCA
 AGGATGAATGTAACTTGGCGCTCGAATGAAAGGAGGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
 CAGGGGACCTCTCGTCACTACTCCCTTAACAACCCACACTGTGGAGCGTACCAAGTGTGTGGCCCGGATGCTCTGG
 GGGCTGTGGCCGCGCTGCCAGCCACTGTGACACTAGCCCATCTCCAGGACTCTCAAGTTAGATGTGCACGACCTG
 ATTGAATGGTGAAGGAAACAGCAGCTCATTTGCCCTCCAGCTGCTGGAGGACCAACCCAGCCAGCTCCG
 TACAGGCTCAACACAGAGTGGCTGGAGGCTCCAGAGTCACTCACTGTCATGCGCTCCAGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGCTATCAAGTGTGCACCTTACAACCCAGTGAACCCAGGAAGTGAANAAC
 TCCGGCTCCAGCGACAGGCTAGCTGTGGCGGCTCCACCGCTGAGGCTGCCCGCATCATCTAACCCCCAGAGGCC
 CAAACCATCATCTGTACCAAGGCGCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGGAACTCCACCCCCAGGGTCT
 ACCTGGGCGAAGGATGGGTCCAGTGTACCGGCTACAAAGACGCGCTTCTGCTGAGCAACCTCTCATCGAC
 ACCACAGCGAGGAGGACTCAGGCACCTACCCTGCTGATGGCCGACAAATGGGGTTGGGACGCGCGGGCAGCGTCT
 ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGTATCCAGCTGTGTCTATCCCTGGGGC
 CAGAGTGCCAGCTTACCTTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCTATCTGCCCGCAGGCTGCTGCTCTCCGCGAGGCGCTGCGCTGCTCAGCATGGGGCTGAGGACGAAGCG
 GTCTACAGTGTCATGGCCGAGAACGAGGTTGGGAGGCCCATGCCGTAGTCCAGCTGGGACCTCCAGGCCAAGC
 ATAACCCAGGCTATGGCAGAGTGTGAGTGGCTACTGGCACCTCTCTGTATACCCCTCAAACCTCGGCACAC
 CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCGAGACCCCAAGCTCAGTGGGGCTGCTTCCCGGAAGTGT
 CCAGGAGGAAGGGGCGAGGGGCTCCCGCGAGGCTCCCATCATCTCAGCTCGGCCGACCTCAAAGACAGAC
 TCTATGAACTGTGTGTGGCGGCTCGGCATGAGGCGAGTGGCCGGCGCACTTCTCTACTATGTGTGTAACAC
 CCGACAGCTGTACAATTTCTCTGAGTTTGCACCTCTCTGGATTTCCAGCGCAGGCTGCTGACCTCT
 ACCAGACTTGAACCCCGGAGCTTTGTATGAAGTGGAGTGGCACTTCAACTCTTGGGCGAGGCGCCAGACGCG
 ATGGTCACTTCCGAAGCTGCAGCGCGGCCAAACCCAGAGATCATGGCCAGCAAGAGCAGACATCCAGAGAGAC
 GACCTTGAGGACGCTCCAGCAGCGCAGCGCAGCCAGACACCGCGGCTCTCCCGCCCAAGCTCCCGACG
 CCCACCATCTCCAGCGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGCTGGGAATGGTGGTTCCTCAAC
 CAGTCTCTTCCGTGTGGAGTACAAGAAGTGAAGAAAGTGGGAGACTGGATTCTGGCCCGCAAGCTACCCCCA
 TCGCGGCTGCTCGGTGGAGTACACGGGCTAGAGAAAGGCACTCTCTACAAGTTTTCAGTTCGGGCTCTGACATCT
 CTGGGGGAGAGCGGAGCGGCCGCGCCCTCTCGGCCCTACGTGGTGTCTGGGCTACACGGCTGCGGTGTACGAGAGG
 CCGTGGCAGTCTCTATATCACTTTCACGGATCGGCTCAATGAGACCACTCATGCTCAAGTGGATGTACATCT
 CCAGCAAGTAAACAACAACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGT
 GACTACAAGAGGATATGTTGGAAGGGGACAAAGTACTGGCACTCCATCAGCCACTCGAGCCAGTGGAGCACTCTCTAC
 GACATTAAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTTCAGCAACGTGATGATCTGTGAGACAAAGCT
 CGGAAGTCTTCTGGCCAGCTCTGTGCACTGCCACCCCACTCTGGGCCCCACAGCGCGGCTCTCTCTGAAACCT
 ATAGCGCGGCTGTGGCACTGGGCGCATGGTGTGCGTCCAGCGACTCCCTATCTGATTGTCTGGGCTGT
 CTGGCTCCATCTGCTCATCATCTCACTTTCACCCCTCTGCTGTGGAGGCTGTGCTTAAGCAAAAACAT
 ACAACAGACTTGGGTTTCTCTGAAGTGCCTTTCACCTCTCTGCCGTATACATGTTGTCATTGGGAGGACTC
 CCAGGCCACAGGCGAGTGGACAGCCCTACCTCAGTGGCATCAGTGGAGCGGCTGTGCTAATGGGATCCACAT
 AATAGGGGCTGCCCTCGCTCGAGTGGGCTACCCGGGCTAGAGCCCAAGCAGCACTGCCAGGCGAGCTCTCAG
 CAGCAGGTGACACCCAGCAGCTGCTGAGCGAGACCCATCTTGGCAATGGATATGACCCCAAGCTCAGCATCT
 ACAGGAGGTCCTCAAGTCTAGCCGCGACGAGGCTCTTCTTATACACACTGCGCCAGCACTCTCACTACACAGTCT
 CTGAGCGCCCATCAGCACTGTGTCGAACGCCAGGAGCAGCTGCTGCTGTGGCCAGTCAAGGTCGAGGAGGCG
 CCGACAGTCTCTGCTTGAAGCAGTGTGGGACCTCCATTTCTCACTCAGGCGCCCATCTGCTTGGGCTGTGTG
 CCAGTTGAAGAGGTGGACGCTCTGACTCTGCCAATGAGTGGAGGAGCTGGTGTGCCAGCAACCCGTAAGG
 GCGTACGTGAGGACAGGAAGCTGGAATGACGCTCTCCCGGCGCACTGGTGGGTGTGCTTTTGAACACCACT
 CTCACAAATTAGGCAGAAGCTGATATCCAGAAAGACTATATATGTTTTTTAAAAAAAAGAGAAAA
 AGAGACAGAGAAATTTGGTATTATTTTCTATATATAGCCATATTGATATTTATGCACTTGTAAATTAATGTA
 TATGTTTATAATCTCAGACACATAGGAGTCTACCCGTTTATGATTTGGAGAGGAAAATAGAGCCCTGCA
 CTTACAGAGACTACCCCGAAGACCAACGACGCTGGCGGGGAGAGCTCTTAACCTGGGCTCTGTGAGT
 CGAGCGAGCTCTCAGGACCAACGATAGCTGGCAAGGAGAGGATCCAGGACATGTGTTATCACAGGTA
 TGAGGAGACAGACGACCGGATCACAGCTGCAGACACCCACAGATGAGTCCGCTGTACGGGAA
 ACATTTTCTCAAGATGCCATGAGAACAGCAAGATGTGTACAGCACTATGAGCATTAATAAACCTTCCAGAT
 CAAATATCCGTGGCAGCATATCTGTAAAAACAACACTGTAACCTTCTAATAAATGTTTAGTCTCCCTGTAAAT

10015386-121201

FIGURE 36

MLRGTMTAWRGMREVTLLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEFP
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALLNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSTGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRNSTAEAAARIYPPAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSOLVIPWGGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCFGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGTGRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNNGGFPIQSFRVEYKCLKKVGDWILATSAIPPSRLSVEITGLEKGTYSKFRV
 RALNMLGESEPSAPSRPYVVSIGYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFIYIYRPTDSDNDSYKDKDMVEGDKYWHSISHLQPETSIDIKMQCNEGGESEFSNVM
 ICETKARKSSGQGRLLPPTLAPPQPLPETIERPVGTMAMVARSSDLPLYLIVGVVLGSIVL
 IIVTFIPFCLWRAWSKQKHTTDLGFPRALPPSCPYTMVPLGGPLGHQASGQPYLSGISGRA
 CANGIHMNRCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLDDSTHQLLQPHHDCCQRQEQAAGVQSGVRRAPDSFVLEAVWDPPFHS
 EPCCLGLVPVEEDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

10015306 "121201

FIGURE 37

CGGGAGGCTGGGTCGTATGATCCGGACCCCATTTGTGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCGCGCAACATGCAGCCCACGGGCGCGAGGGTTCCCGCGC
 GCTCAGCGCGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC
 AGCCTCTTACCACGCGGGGTGTCCCCAGCGCCTCACTACCCAGGCCCTCACTACGCCAGG
 CACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCCACTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTCTACTCTGAACCTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTCAGACAC
 CACATGTACACCAACGTGACGGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTGTCTTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGAAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTTCAATGCCT
 CCCCATACCTTGTTCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC
 TGCTGAACAGCTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGAAAAA

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FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
 ><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
 ><MW: 53569.32, pI: 7.68, NX(S/T): 5
 MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS
 ALTTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
 TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
 QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCTPWAESSTKFRHHMYTNVSGLT
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVSQAPVIFSHSAARAVCDNLLNVPDDILQL
 LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGNYDGTGRFPQGLEDV
 STYPVLIEELLSRXWSEEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
 SHLVPQNGHQATHLEVTQPTNRVPWRSSNASPYLVPGLVAAATIPFTTQWLC

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

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FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCACGCAAGCCTGATAAGCAATG
 AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGTCTGGTGCCCCAGCTGAAGCCAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGTCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTTCATCATTGTCTACCTGTCCGTGGTGGGTGCCCTGTGTCTCT
 ACATGGCCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCTTGAGCGGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGATGGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCTTAACCTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTTCGAGGCGGCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTTGGAAGATAAAGCTGGGTCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCCCTTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTTCAGGGTGCAGTGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCTGTACTTGGGTGCCTCTTGTCCCTGAACCTCGTTGTACCACTGCATGGA
 GAGAAATTTTGCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTTCTCTCA

1005336.121201

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGGCLVPPAEANKSSIEDIRCKICPPYRNISGHIYNQNVQSQKDCNCLHVVEFM
PVGHDVEAYCLCECRYEERSTTTIKVIIVYISLVGALLYMAFLMLVDPLIRKPDAYTE
PLVNEEENEDARSMAAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Signal peptide:

amino acids 1-20

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTCGAGGCGTGAGACTGAGTTCATAGGGTCTCTGGGTCCTCCCGA
 ACCAGGAAGGGTTGAGGGAACAACTCTGCAAGCCCCCGCGACCCCAAGTGAGGGGCCCGGTGTTGGGGTCTCTCC
 TCCCTTTGCATTTCCACCCCTCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGCGCGCGTTGATG
 CGGAGCAAGGATTCGTCTGTCTGCTCTCTACTGGCCCGGCTGCTGATGTTGGAGAGCTACACAGATCGGCAGT
 TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCTGTGTACGGCCGCAATCGATCTGCG
 GGCATTACCAAGGACTGGCATTTCGGCGGCAGTAAAGAGGGCAAAACCTGGGGCAGGCCTACCCCTGTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCTTGATGGTGTGTCGGAGA
 AAAAAGAGCGCTGCCACGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATATGGCATCTGTATCCGAGTT
 ACTGAAAGCACTCTTAAACCTCATCTCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAAGCGTCATTAC
 TCAAACCATGACTTGGGATGGCAGAACTCTAGGAAGACCACACTAAGATGTACATATAAAGGGCATGAAGGA
 GACCCCTGCTTACGATCATCAGACTGCATTAAGGGTTTTGGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
 CCAGTGCTCCATCAGGGGGAAGCTGTGACCAAAACACGCAAGAGGGTTCTCATGGGCTGGAAATTTCCAGCGT
 TGCAGCTGTGCGAAGGCGCTGCTTGCAAAAGTATGGAAGATGCCACTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATTAAGGTTCAAGTGCAGAGAAATGGCTAAAAATAAGAAACGTGATAGAAATATAGATGATCAAA
 AAAGGGAGAAAAGAAACATGAACTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
 CAACTTGTCTATGTAAATATGTACACATTTGTGGAATAATGCTATTATTAAAGAGAACAGCACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTTCCCTTCAGATTGCTGATGCT
 TTATACAAATAACCTACATGCCAGATTTCTATTCACAGTTAGAGTTTAAACAAAATACTCTAGAAATACTTGTGA
 TACAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTTGTTAATTTACACAGAAAT
 TACCTTTTGATTTGTAACACTACTTTCTGCTGTTCATCAAGAGTCTTGGTAGATAGAAAAAAATCAGTCAATAT
 TTTCCAAATAATTGCAAAATATGAGCCAGTTGTTTAGGAAGGCCCTTTAGGAAGACAAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTCTC
 TTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCCTGCTGATGCTTATATTTTCCA
 AACTATACCCATAAATTTGACTAGTAAATACTTACACAGAGCAGAAATTTTACAGATGGCAAAAAATTTTAA
 GATGCTCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTAATTTCTTAAAGATTTGGCCATTAACCTATATTT
 GATAGAATTAGATTGGTAAATACATGATTCATACATACTCTGTGGTAAAGAGACTTAAGCTGGATCTGTACTGT
 CACTGGAGTAAGCAAGAAATTTGGGAAAACCTTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGCTG
 AGGCACAAGTTGGCTGTTCATCTTTGAAACAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATAATTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCGTAATCTTCAAAATTAATTTATTTTATAG
 TGTCTGAGATCCTCAATATATCTCAATTTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
 TTTCAATTGCCCTCTATAAGCTTCTGACTAGCCAAATGGCATCATCCAATTTTCTCCCAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGCGTAGTTTCGGTTTTCTGCAGCCATTCGCGTTAAAAAATAAAGTAGGATAACTTGTAAA
 AACTGCATATTGCTAATCTATAGACACACAGTTTCTAAATCTTTGAAACCACTTTTACTCTTTTAAAACTT
 AACTCAGTTCTAACTTTTGTCTGGAGCAGAAAACATAAAAGGTTATCTTATAGTCTGACTTTTAACTTTT
 TAGACCACAAATCACTTTTGTGTTTTCTTTACTTAAATCCCATCTGCAGTCTCAAATTAAGTTCTCCAGTAG
 AGATTGAGTTTGACGCTGTATATCTATTAATAATTTCAACTTCCACATATATTAACTAAGATGATTAAAGCTTA
 CATTTTCTGCACAGGCTGCAAAACAAAAATTAATAACTAGTCCATCCAAAGAACCAAGTTTGTATAAACAGGT
 TGTCTAAAGCTGTGAAATGAAATGAAACATTTCAATCAACATTTTCTATAGTAACAATTTATATATTTACAAT
 TTGGTTTCTGCAATATTTTCTTATGTGCCCTTTTAAATAATTTATTTAGAGTAATTTTGAAGCAAGAAATG
 TTAATGAGATGTATTTCTTATAGAGATATTTCTACGAAAGCTTTGTAGCAGAAATATTTTGACAGCTATTGAC
 TTTGTAATTTAGCAAAAATGTATAAAGATAAAATCTATTAATTTTCTCCTCTAAAAACTGAAAAAATAA
 AAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

1001536.121201

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTTGGCCTCCCCAA
 GTGTTGGGATTACAGCGGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATCTGTTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGACCACCAAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAATACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCCTCAGTCCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTCTTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
 CCTGGTTTGGAGTCCTTTCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAAACACATCAAATTTGCTAAGCGGGCGGATACCCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTCTATGGCTGGTGGCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAACCAACAGTTGGTCAATGGCTCATTCGTTAAAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCCAATCAGACTGCACCACAAGTCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATTAATCCCAGTGCTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAACACACCTGGGCAACATGGTGAAACTC
 TGTCTCTACTAAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

1005336 "121201"

FIGURE 44

MCFKALGRNSVLLRICALFIPLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVFP
PGLESFSPQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQKRIAHVMWKTVPVQWLIR

Signal peptide:

amino acids 1-24

100536121201

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGCGCTGCCATCCCGAATCCTGCT
 TTGGAACCTTGTGCTTCTGCAGAGCTCTGCTGTTCTCTCGACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTTGGAGTCAACGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCAGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTACTGCGTATCGAGCCGTGGAGGTGCGCGACGAGGGCACCTACTCTGCCACCTGCAC
 CACCATTACTGTGGCTGCACGAACGCGCGTCTTCCACCTGACGGTCGCGGAACCCACGSC
 GGAGCCGCCCCCGGGGCTCTCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGTACTGGTCAC
 TGTCTCTTGGCCGCCCGCAGGCGCCGCGGAGGTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCTTCCAGCGGCTGGTCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCAGGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGTCAGCCTCGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
 AAAAA

10015336 "121201

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
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MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDDL
YASGERRAYGPLFLDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPFPRGSPNGSSSHSGAPGPDPTLARGHNVINVI VEPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDLDKGFRKENCK
```

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coroporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGGCGCTGGCGCAGCGGCAGAC**ATG**GCCGTGTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCGAGGAGGC
ACTGCTTGAGAAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGA
GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG
TGCCCTCCATGCTGTGCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGCTCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACCTGGTGAA
GGTGGACACTTCTCTGACCCGCTGGTTTTTTTTTGGCGTCACCATGTCTGCATGGTGATCC
TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGCGGCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA
GGACTCCCTCAGTGCCCTTCGGTGGCTCCAGATTCAATTGATTTCCACACACCCCCCTCTCC
GCCCCATCTGAAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGCTCTTCTTATCACC
AGCCTCATCTACCCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTCTGTACAACCTTTGCTGACCTAT
GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGGCCAACAGCAAGGGGCTCCCAGGG
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACACCAGCCCCGGGT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGTGG
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCTTAAGATTGTGCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCTCCTGGTGCACTCATCT**TAGA**AGGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCCATTCGGTGCAAGGCAGATATTCAGTCAATATTACAGAACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCACGCTGCGCTCATTCAGCT
GACAGCGAGATGCAAGCAAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCTGGCATGGTCAGTCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
CGGGGTGAACAACCTGCCCACTAACAGACTGGAAGAACCCAGAAAGATGGCCCTTCCATGAAT
GCTTCATTCCAGAGGGACAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTCTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAA

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FIGURE 48

MAVVSDDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGGLQRPEDRFCGTYIIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGly
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITSLIYPVCTNIESLNKGSGSLWTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

10015366 1213001
 102121 9855001

FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRII
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGVALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDMSEDGFFYLSFAEALR
AHSCLSDRLOYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQCPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPPFWREEHIEGG
HSNTDRPSRMIFYPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

10015336.121201

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGCTGGGGACACTCTGGGCGGGCCTTCTGCCTGCAT
 GAGCGCTCTGAAGCCACCTGTCTCTGGAGGAACACAGAGCGAGGGAAGAGGACAGGACTCGTGTGGCAGGAA
 GAATCAGAGCGGGGAAGCCCCATTCACTAGAAGCACTGAGAGATCGGCGCCCTCGCAGGGTCTGAATTTCTCT
 GCTGCTGTTACAAAGATGCTTTTATCTTTAACTTTTGTCTTCCCACTTCGACCCCGGGCTTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTCTTGTGGCTGATCACCAGACCTCAACCGCTCTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGCGGAAGGGGTTTCCCAAGAAACAATGACCTTAAACAAGTTGCTG
 CTCTCAGATGCCAAGACTATGATGAGGTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCGCTGTTGGG
 ATATAGAAACCAACAGCCGCTACAGATGGCTATCTTACAACAGGCTGTCTGATAGACAGAGTACCTGGGTTC
 CTGCTCTTTGACATAAGGCTTATAATCATCACCAGACCACTTTGTCCGCTCTTTGCTCAGAATAGGCCAGGCTG
 GATCATCTCCGAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACAACCTGGGACAGAAAC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATTGGTGTCTGTGACACACCCCAAGAGCATTTGGTGTGAT
 AGGGAATGATAGAAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGAGACCCCTTGTGATGATGACCTGAA
 GCAAGAGGGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCCAAGAGCACTTCAG
 AAAACCTGTGCTCTTAGCCCCAGAAGACCTGAGCGTCACTGCTTCAACAGTGGGACACAGGTGACCCCAAGG
 AGCCATGATAACCCATCAAAATATTGTTCAAAATGCTGCTGCCCTTCTCAAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTCTGGCTCATATGTTGAGAGGATGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATGTTTCCCGGGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACOCCT
 GAAGAAGTTCTTGTGAAGCTGGCTGTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGACAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTCTGTGTAATTTGCTCATGGAGC
 TGCCCCCATGTCCAATTCACTCATGACATCTTCCGGGAGCAATGGGATGTGAGGTGTATGAAGCTTATGGTCA
 AACAGAATGCACAGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTCAAGTTGGGGTGCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAATCTTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGTGGCTG
 GCTTACACAGGAGACATTTGGTGGCTGGCTCCGAATGGAATCTGAAGATCATCGACCGTAAAAAGAACATTTT
 CAAGCTGGCCCAAGGAGATACATTGCACCAGAGAAGATAGAAAATATCTACACAGGAGTCAACCAAGTGTAC
 AATTTTGTACACGGGAGAGCTTACGGTCACTCTTAGTAGGAGTGGTGGTCTCTGACACAGATGTACTTCCCTC
 ATTTGACGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAAGTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
 AGAAGACTTGCAGAAAATTTGGGAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAAAGCGAGGAGGCTTTCCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATAGGATAAGTACTTAACTAGCTGCCGCCCACTG
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 GAGCCAGTCTTGTCTGTCTTCTTCTTCTCATGATTCCAACCTTAATCATTTAGTAGAACCAAGTCTCAAGGCT
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 TCCTTCTACTGTTCAAACATAAGAGATTTTAAATCTGAAAAACCTGCTACATATCATGTTTCTGACGACTCCAC
 AAACCATAAATTTTAGTTTATGCTATCACTCATGTCAATCATCTATGACACACATGCTCCGATGCTCTT
 CTGCTTAATTAATTTGTACTGAAGGAAAAGTTTGAATACATAAACTTCTTAACTCTCTAGTTAGATA
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 CAGTAGGACTGGGGAGTAAATCTGTTCCCTACAGTTTGTGCTGTGAGCTGGAAGCTGTGGGGGAAGGATGACA
 GGTGGGCCAGTGACTTTTCCATTAATGAAGCAAGCACTGATAAAAAACCTCTGAACCTGGGAACCAAGATCT
 ACAGGCAAGCAAGATGCCACACACAGGCTTATTTCTGTGAAGAACCACTGATCTCCCCACCCTTGGATT
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 TATTACAGATAAAAA

10015386.121201

FIGURE 52

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CCFSDAKTMVEVFQRGLAVSDNGFCLGYRKPNQPYRWLSYQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWII SELACYTYSMVAVPLYDTLGPFAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCV E HAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKEQLQKGIIRHDSFWDKLIFAKIQDSLGGRRVRIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVP LACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPV LQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTL KAKRGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

102121" 9855001

ACGGCGGAGGGCCGCGCCGAGCCGGGGCCGAGCAGTAGAGGGCCCTAGCGGGGCCGAGCGGGG
CCGGGGCCCCCTAAGCCATCTCTGAAGTCATGGCTGCCCAGGACATGGTGAACCCGCCAAT
CCGGTATGCGACAGCTGAAGGCCAGGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
AGCTGGTACCTTACCTGGGAAGTATAAACTGACAAACAGCGGGCCCTCGGAGAGATTCTGTCA
GACAGGGCCCGTGGTCTTTCTCGTGGTGACTGTCATTGCTCAATATCAAGTTGATCTGGACA
CTCGCGGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGCTATGATGAGGCC
CTAGGCCGCGCTGGAGCCCCAGGCGCAGAGGCGAGTGGTGGTCCCGCGGGTCTGGACGTAGA
GGTGTATTCAAGTCGACGAAAGGATATATTGGGACGTGATGACCAACCGTGTGGAGGAT
AGGCCCGGGGAGCGAGGCCCGGGGCATCCATGTCTATGTCTCAACGAGCCACGGGCCACGT
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TCAAGGACACAGCCAAAGCTCTGCTGAGAGCGCTGGGACCGGCTGGGCTGGCCCTGCCG
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TAAGTCACCTGCGCCTCTCTTCTGGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTTGA
GCTCAGCAGAGAGGCGATGCTGCCATCTGGGCACACAGAGCTGAACCTCTCGCCCGCGGCC
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GGAACCCACCCAATTACTGTCTACAGATGCTGCGCTCTGCTTTGACCCAGGGGTGTCT
CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
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CTGGAGAGGAGTACAGCCCTGTACTGCTCTGCTCGGTAATGACCAAGGGTATGAACACA
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GAAGAAGAAGCTTATGAAGGTGAAGTTACAGGCTGCTCAGGCTGAGGTTCTGGACC
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ATGACAGCTCTCTCCAGGACCTCTGGGGGTGGGTACTGCTGTAACCCAGCTGGCTAGGCTTCC
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TGAGACTTAATTACTAAGTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT
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ATCTCCAGCAGCTCATCTGCCCTTTGAATACCTCACTTTCCAGGCTGGCTCAGAACTCA
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GACACTGGCCAGGCGCTCCTCTCAGCCTCTCTTTGTCCAGATTTCCAAAGCTGGAATAAGTT
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FIGURE 54

```
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REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTHAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNNRRRRRFC SKVEGYGVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKKHFNTVPGVQLRNVDLSLKKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDFFTWTQLAKCLHIWDLVDRGNHRLWLRLFRKKNH
FLVVGVPASPYSVKKPPSVTFIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

101536-12101

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACTTAAGCACCATTAAAGCCCACTGGAAATTTGTTGTCTAGTGGTTGGGGTGAATTA
 AAGGAGGGCAGAAATGGATGATTTCATCTCCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGGCTGTTAATTTCTCAGAGGAACGACGTAAGCTGGTGACTGTTTGG
 GTGCTGGCCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTTGAGGGAACACCACCAGCAAGTGAACACATAATGTGATTGTCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCCTATATTTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGGTAACCTCCATGTCATTCT
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 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCCTTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTTAGACTGAGTAAGAGCAGTAAAGAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
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 GGTTCTGGGTTGCTCTACCTCTCATCTCTGTCAGTAGGACACGACATTAATGTTCAAGGTCCAGC
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 TCTTGTCTCAGCTTGGCCTCTCATCATGTATTTCTAGAGTCCAGGGGAGGTGAGGTTAAAACTTG
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 GACTGGTGTAGACTTTAGGTTTCATCTAGTCCTTCAAACATATATGTTGCTAGATTCTCTCTGGA
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGCAAAAAAAA

10015386.121201

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

10015366 121201

FIGURE 57

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAATTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGTGCAAGACCAAGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGGAAGGAAACGTGCTTGGTAACAGCAA
 GTCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG
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 AATCATACACTCTGAATTGAAGTGAATCACATATTTCAACAAGGGCCGAAGAGATGACTA
 TAAATGTTCTGAGGGACTGAATACTGAAAAGTGTGAATGTACTAAATAAATGTACATCTGA

1005366.121201

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRRVRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLOAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

10015336.121201

FIGURE 59

GGATG CAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGCTGCTTCTCTTCTACGCTGGCATTGCCCTCTCA
 CCAGTGGCTTCTGCTCACCCTGTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
 TGCCATTGGGGGAGCCAGGAAACCTGGGCTGCTGGATGGCTTCCCATTTCGCGGGTGTGTTGGTGCTGA
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 TCCCTGGGCAAACTAAGCTCCTTGCAGGATCCTGGAGATTACGCCACCCTCAGCCGCTTCCCGATCTCAGG
 TTGACCCCTCTACACCACCATCAGCAGCCTCAAGGCCCTCAGCACTGGCTCACTGCCTACCTTTATTGATGCTG
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 TCTTTTGGGCTCATTCATCTGCTGCTGTTGTCCAGCTTCACTGGGAGGGCCAGCTGTTCCACCTAAGCTAC
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 TGTACTCAACTCTGATTTTGGATCTGAGGCAAGAGGGGCGGCTCTCCGAATGGAATAAAATAGGCGCG
 GCGTGTGACTTGCACCTATAATCCGACACTTTGGGAGGCAGAGTGGGAGGATTGCTTGTGCTCCAGAGGCTCA
 AGACAGCTGTGGACATAACAGACCCGCTCTACTATTAAAAAAGAGTGAATAAATGATATAT

1015366.121201

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
 <subunit 1 of 1, 1089 aa, 1 stop
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 VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLF
 PGAFSKAFFFPSENVRLDLDTVNGILEHLYPTMDSGEWDVLIHFLGVDHCCHKHGHHPHEM
 AKKLSQMDQVIQGLVERLENDTLVVAGDHGTTNGDHGGDSELEVSAALFLYSPTAVFPST
 PPEEPEVIPQVSLVPTLALLGLPIPFNGIGEVMAEFSGGEDSQPHSSALAQASALHLNAQ
 QVSRFLHTYSAATQDLQAKELHQLQNLFASKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
 ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAI SPGFPCPLLLTPVAWGLVGAIA
 YAGLLGTIELKLDLVLGAVAAVSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA
 VFFSDSFVVAEARATPFLGGSFILLVVLHWEQQLLPKLLTMPRLGTSATTNPPRHNGAY
 ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPPLASVMGGRKNLWYGACVAALVALLA
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLVSGASMVLP
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
 EFRGRLETRKSGQLPTVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQSFLL
 LLHLLAAGIPVTPGPTVPWQAVSAWALMATQTFYSTGHQPVFVAIHWHAAAFVGFPEGHGS
 CTWLPALLVGANTFASHLLFVAGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEEP
 LMEMRLRDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWKVFAPKFI FEAVG
 FIVSSVGLLGLIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

102421 9955001

FIGURE 61

TGCCGCTGCCGCCGTGCTGCTGTTGCTCCTGGCGCGCCTTGGGGACGGGCAGTTCCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGCAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCACTGGCTGGAGCCGAACACTCTTACTGCGT
 ACACGTGGAGTCTTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTCCTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA
 GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTATCACCCCTCAATATCTCGGATGAT
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAAACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCCTGACATTTGTGCGGGGCCCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTTGGTCGACTGGGATCCCC
 AAACGTCAGGCTGTGTATTCTTCTGCTGTTCAGCTTCGACCAGGATTACAGAGGCTGCGAG
 CCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGGAACTGATGCCAACACTTCCTTTTGCTTTTGTTTCTGTGCAAC
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT
 TTGTGAGTGTCTGTGAGAATTACTTATTTCTTTTCTATTTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCCTCTGGAGTCCAGGGGCTGGCCGGT
 TGTTCATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGG
 TGGGTGT

1005366.12120

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPPIRRAPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFED
KRFFVPAEKIVINFITLNISSDKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEEFAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

10015336.121201

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACTCACTGCGGA
GGCTTCTGCTGCGAGCCCGTGGGTGGTCTCGGCCGCCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGGGCGCCCCACGTCTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGCGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGGCACCCCAAGACCCCGAC
GTGTACACGAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCCTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAAGGTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

101536 121301

FIGURE 64

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTTCGGCGCTGGGGACGGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAACCTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACGAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAGCCGCCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGCGCTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCCGAGGAACGGCGGATGTT
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCTCCCGAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCGCTGTGCTGTGCCAGCAGGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTTCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTGATCCC
 GAGTTGAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGA
 TTGCCTGGGACTCCACCTTCTATCAATCTCATGGTAGTCCAAACTGCAGACTCTCAAA
 TTGCTCATTT

1005366.12101

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGSVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGCTGCGGCTCGGGGCGACAGCTTCTCGGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAAGGTACTTTCTTTGTCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTGTGCATTTACTCTCATCAAACGCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGGCTGTGAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGCTTGAATATGAAAGGCTTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTATCCAGAGGCCAATATACCCACCTGCAGACCAGAGACCTACGAGGGGC
 TATGTACAGCCCTGGGTTCCCGAGCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCTAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTCACTCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA
 CCACCGCATTTGCTGCCCTCAGGCTTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTCCACCAAGC
 AGCCCCCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTTCATCTATGCCAACCTCAGCGTGCCCTGTGGTTAGGA
 ATGCAGCACTGTTTGGTGGAACTTGACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
 ACAGGAATCCCGAGACCCCTGCAGCTCCAGCCCTGAAGACT**GTA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGACGCTTTGTCTGTGCCTCGCAATCAGAGGC
 AAGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTGTATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCCTGAGAGGGAAGTTTCTGG
 AGTTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGCATCAGTGGGCTC
 TTTTGGCACTTTGAACCTTGACCAAGGACCAAGAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTAAAA
 ATGTTTATAAATCAAA

10015386-121201

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRQLQDVYMLNVKGLARGVFQRVTSAITDLSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 OPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW
 NLHRSGEGSDSTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

amino acids 1-19

1015336.121201

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCTGCTCCATCTCAGGAGCCCTGCTCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGTGGCTGAGGGACCGAGCCGAGAGCCCCGAGCCCCGTAAACCGCGCGGGGAG
 CGCCACGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCTACCTC
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCTT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTAAAGTGCCCTTC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCTCATGTTTATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTATGTACATCCTTGGGAT
 CTGCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAATATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACTACCCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCTGTGTGTAGTCCCACGGCCTCTGCCTC
 CCCAGGGAGCAGACCTGGGCCTCCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC
 CTCTTCTCAGCCTCCACAGTGCCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGCCTA
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATCTTGCCCTTCCCCAACAGGTTTGTAA
 TCAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAA

1005336.121201

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFVWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILLGGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQITIDFL
NDNIRRGIEYDDLDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAVIWFMNDNYTIMACILGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

1001536 121201
102121 985500

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGA
 CACCTGGGAAGATGCGCCGCCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCGCCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACGTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCATAAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCCTGTTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
 GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCTGTGAAAAA

1005336.121201

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
```

```
><subunit 1 of 1, 484 aa, 1 stop
```

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNHATSILQQLPILLSAM
REKPAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTWKFNNASAASLTMPITLDNIPFSLIVSQDVVKAAVAASLPPEEFMVLLDSVL
PESAHLRKSSIGLINEAKADLKGSTQIVKILTQDTEFFIDQGHQKAPQLVILEVFPSEAL
RPLFTLGIEASSEAGFYTKGDLILNLNNISDRIQLMNSGIGWAKPVDVLKNIITEI IHSIL
PLPNONGKSGVPSVLKGLGFEAAESSITKDALVLPASLWKPPSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACA**ATG**GCGAGCGCTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTGCAGCGTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTGTTTGCAGCAAGCTGATGAAGAATTCCAGATCCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACACGGATATTTTTTGGCATGGTGGATTTTG
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCACTCCAACTTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCATATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAAAGTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGGCTTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTTCTGATGAGT**TAAAA**AGGTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCTTTTGGAGTAGAGAAATATGTGTGTCATGTGGTCTTCTGAAAAATG
 GAACACCAATCTTCAGAGCACACGCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTTCAGATTCAATCCATCTCCTTAGTTTCTTTTAAAGGTGACCCATCTGTGATAAAAAAT
 TAGCTTAGTGCTAAAACTAGTGAACCTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTTCAGAGTTTCGAGACCATTCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
 AAAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCACGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGTTTTCAGTGAGCCGAGATCACGCCACTGCATCTC
 AGCCTGGCAACGAGCGAGACTCCATCTCAAAAAAAGAAAAA

10015735.121201

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTKRPFVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

10015386.121201

[illegible]

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

10015361240
10015361240
10015361240

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGAGCAGTCCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCAGAGGCATACCCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGAGGGCCTCCTGGGATTCAATTCCTGTTCCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGCAGGGT
 ATGTCT**TGAA**AGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTC
 CCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTTGCCCTCTGTTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
 ACTGACCCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAAGTAAATAAACCATCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

1005336.124201

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVG YILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTS SAISSLACIISVVGM RCTVFCQESRAKDRVAVAGGVF
FILGGLGFIPVAWN LHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQRRNSNYDAYQAQPLATRSSPRGPQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

10015336.121201

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAAGACATAGAAAAGAAATCAACTTTCCTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

10015336.121201

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

1005386-121201

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACCTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCAGCTTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTGCGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACAACTCAACTGCCCACCTTCATT
CTGTGACCTGTCTGAGGCCACCTGCGAGTGCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCAAGGCTGGCTGGGGAACCCCTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

10015306-121201

FIGURE 82

MAPRGCI VAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

10015386-121201

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGCGCCGCTCCCGCCGCTCCCGGACCAGAAAGTTCTCTCT
 GCGCGTCCGACGGCGACATGGGGCGTCCCCACGGCCCTGGAGGCCGCGAGCTGGCGCTGGGGA
 TCCTTGTCTTTCGCTCTCTTCTGGTGCCTCCCTAGGTCCGCTGGCAGCCTTCAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGCGACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCCGCCCCATCCGCAACCTCACGTTCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
 GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGCT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTAAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCGAGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGCGGATGGACAGCAACATTCAAGGGATTGAAACCC
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGGCGCATCTGCTTTCGGAGCCACAGC
 CCCCCTGTCTCTCCAGGCCCCGAGACGTCTTCTTCCATCCCTGGACCTGTCCCTGACT
 CTCCAAACCTTTGAGGTCATCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GCGAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCTGCTCTGGGCTCAGATACTGTGACATCCCAAGGCCAGCCCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGTGCTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCAGCCCTTCAGCAGCTCTCGTTCAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCTCCAGGCACCAGACACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCTTGGCTCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCAGGCTGCTGCCCACATGGCCATCGCC
 ACCTTCCCCAGCTGCCCTCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCTCCGTGAGCAAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGTGGTGGGGCCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGCTTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGAT
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

1005386 "121201

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTTCCACCTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCC
 TTTCTGCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGA
 CTCGCTCCCCGACCAGCGGCCTGACCTGGGAAAGGATGTTCCCGAGGTGAGGGTCTCTC
 TCCTCTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTACCCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAGTGTGTGGAACCTCACACTCCCTCTGGAAGTCCGGGCCCCACCAAAGTCTTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCGCTGCCTTCGGCCCTTGCCCTG
 CATCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCCAGAGGACAAA
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACTGCGTCGCTTGGCCCTGGAACACGAGG
 CCTCGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC
 GAAGTCACTGGAACGTCTTCTAGCCAGACCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAAACAGTTCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

1015366 "121201

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLGLLWFPPLDSHARARFDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSGCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPDG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

1001536.121201

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATGG**ATTCCCTGCGGAAAATGCTGATCTCAGT
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
 AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
 CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCGT**T**
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC
 TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
 TCCTGTGAGCTGCCGTGCGGTGAGCACGTTTCCCCAAACCTGGACTGACTGCTTTAAGGT
 CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACCAATAAAA
 TCATGTTCTCCAAA
 AAAAAAAAAA

101536 121201
 101536 121201

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

10015386.121201

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAGCTAACCCCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTCTTACTCTGGCACCACCTCTCCAGGCTGCGCATGGGGCCAGCACC
 CCTCTCCTCATCTTGTTCCTTTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCCTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGAAGAAGGAATGAGAAGTAC
 GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGGCACAGAATGACACAGCCTTTGTCTTCCAAGGCTGCGTGACTTCACCCTT
 GCCATGGCTGCCCGGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCTTGGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTTCTTTATTTTGGCTCGGAGGCCCTCCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAAACACTTTGCAGCTAATCAAATCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTTCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA
 TGTCCCAGAGAGAATGCTGAGGCTGCCTTTGTCTATCTGTGGGACCCTCTATGTCGTCTATAA
 CACCCGTCTGCCAGTCGGGCCCGCATCCAGTGCTCCTTTGATGCCAGCGGCACCCCTGACCC
 CTGAACGGGCAGCACTCCCTTATTTTCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT
 AACCCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAGAGGAGGAGGTTTGAAGGAGCTAGCCTTGTTTTTTGCATCTTTCTCACTC
 CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCTCATTCTTCAAATGTGGGCCAG
 TTGTGGCTCAAATCCTCTATATTTTAGCCAATGGCAATCAAATCTTTTCAGCTCCTTTGTT
 TCATACGGAACCTCAGATCCTGAGTAATCCTTTTAGAGCCGGAAGAGTCAAAACCCCTCAATG
 TTCCCTCCTGCTCTCCTGCCCATGTCAACAAATTTTCAGGCTAAGGATGCCCCAGACCCAGG
 GCTCTAACCTTGTATGCGGGCAGGCCAGGGAGCAGGCAGAGTGTCTTCCCTCAGAGTG
 ACTTGGGAGGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCTCTCTCTCACTCCTCCCT
 TCAGTGTCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCATTAA
 AGGAAATCCACAAA
 AAAAAAAAAAAAAAAAAAAAAA

1005386.121201

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWSGPLQGQHHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPFVWGTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAGEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTQ
QWDTPCPRENAEAAFVICGLTYVVYINTRPASRARIQCSFDASGTLTPERAALPYFPFRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

102121" 0855001
1001530 121201

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGCTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAAGCTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTGAGTCCTCGGGCTGGTTCCCCCGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATCCAGTGGAAAAATCCAGCGGAAGTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAAGAGTGTGTTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCACTCCCTTATTTATACCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAATCCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCTCAGAGCAACCACGCCCTTCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

1005336.121201

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPRTAKWKGPQGDLSTDSRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELEDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATT PFLP
 RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

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FIGURE 93

GC GATGGTGC GCCCGTGG CGGTGG CGCGCGCGGTGCGGAGGCTTCCTTGGTTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
 C**ATG**AGGAGCCTGCCGAGCCTGGGCGGCCCTCGCCCTGTTGTGCTGCGCCGCGCGCCGCCCGC
 CCGTCGCCTCAGCCCGCTCGGCGGGGAATGTCAACGGTGGCGCGGGGCGCGCGGGCAGGTG
 GACGCGTGCGCCGGGCCCGGGTTCGGGGCGAGCCAGCCAGCCACCCTTCCCTAGGGCGACGGC
 TCCCACGGCCAGGCCCGGAGGACCGGGCCCCGCGCGCCACCCTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGAGACCAACCCCTTTGGCGCACTGCTGGACCCCTCTTCC
 ACCACCTTTCAGCGCGCTCGGCCCCCTCGCCGACCAACCCCTCCGGCGGGGGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAACCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG
 CGCGGACCAACCCCTGTAGCGACACCGTACCGGCGCCACGACTCCCCGACCCCGACCCCC
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACAGACCACAGGCGAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
 TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTACGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACCTGAAGTTTATT
 TTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT
 TATATTTAATGTCAAGATTTAAAAACATCTAATTTACTGATTTTAGTTCCTCAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTTATTGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGACCAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTGCTTGTACTGCACTGAAAGTAATTATTCTTTGACCT
 TATGTGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCCCTTCACTGAGCTGTTTCTTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACCTCAATAAA
 TTCTGGTTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAAAGAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTACTGTTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
 AGGCTTGGCGCGGTGGCTCAGCCCTGTAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCGTCTCTACTAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCCAGCTACTCGGAGGCT
 GAGGAGGAGAAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
 GCACCTCAGCCTGGTGAGAGAGGAGACTCTGTCTTAAAAA

1015386.121201

FIGURE 94

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLSGGLALLCCAAAAAASVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPPLWATAGPSSSTTFQAPLGPSPPTPPAAERTS
TTSQAPTRPAPPTLSTTTGPAPTTPVATTVPAPTTPRTPTPDLFPSSSNSSVLPTPPATEAPS
SPPEYVNCNSVVGSLNVNRCNQTTGQCECRPGYQGLHCETKEGFYLYNTSGLCQPCDCSP
HGALSI PCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTACAGTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

1015326.12401

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRDLDPQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRITLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

10015336.121201

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTTACCCTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATTGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCGGGGTGCTGGAGCTGCCTTGGTGACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTTCGTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTAGCCT
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATGAGAAATGCAGAGACTCACCCTGATTGAGGGATCACAGCCCCCTCCAGGCAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

101536 "121201

MLLLLLP LLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETDRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTTHRENILPGTLESGCPQNLTCSPWFACEQGTFFMISWIGTSVS
PLDPSTTRSSVLTILIPQPDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTMTVFQGDG
TVSTVLGNSSSLSPPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQSPSNPGVLELPWV
HLRDAAEFTCAQGNPLGSGQQVYLVNLSQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRS
CRKKSAPAAAGVNDGTIEDANAVRGSASQGLTEPWAEDSPDPQPPASARSSVGEGLQYA
SLFSQMVKFWD SRGQETADTEYSEKIHR

amino acids 1-15

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCCTGTTCCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCAGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCGGGTCTGCACCTCCAGAGCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTCCCCCAA

1005336.124201

FIGURE 100

<subunit 1 of 1, 170 aa, 1 stop

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVS PVKVTALGGGKL

MGKLVGRNSDTNREAL EEFKKLVQRKGLSEEDI FTPLQTGSCVPEH

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
 GCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTAGCACCA
 GAAGTGTGAGAACGCCTACCCCGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACAGTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTCCACTTGGTGTGGTTCCTGTTCACTCTGTAAAT
 AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACCTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTTCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

1015355 "121201
 1015355 "121201

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHNRNDIMLVKMASPVSITW
 AVRPLTLSSRCVTAGTSCISGWGSTSSPQLRLPHTLRCANITIIIEHQKCNAYPGNITDTM
 VCASVQEGGKDSCQGDGGFLVCNQLQGIISWQDPCAITRKPGVYTKVKYKVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCCTATTTCAGATTTCATTGTTT
 TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
 GTGAAAATAGAAGTTTTTGCATCGTCCAGAAAACTGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
 AGATTGAACCTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAAGATATTTTAAAGA
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
 GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTTGA
 TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1015386.121201
 1015386.121201

FIGURE 104

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTKSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNHDHGDGFISPKEYNVYQHDEL

```

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCTCCCAAATAA
AGTACTTATATTCTC

1015336.121201

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:

amino acids 1-18

1015385-121201

FIGURE 107

CAAGCAGGTCATCCCCCTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCTTGGTGTGTGGGGGA
 GTCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGCCCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTGTTGGCCTGGGAACTTCTTGGAACCTT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

1071536.121201
 1071536.121201

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPFVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPQGQDACQGDGGPLVCGGVLQGLVSWGSGVPCGQDGI PGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

10015386.121201

FIGURE 109

GCGGGCCACACGCAGCTAGCCGGAGCCCGGACCAAGGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCCTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCC**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGAATCC
 TGAGCCTTGGGTCCCCCTCCTCTCTTCTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAAAGTAGAGGGGCGAGGGCCAGGCGAGGAGGCTTCCAGCCTGTGTTCCC
 CTCCTTGGAGGAACAGCACTCTCCATCCTTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCAGTGCTCTGGTGTCAACC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGAAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGTTGCTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

1015386-121201

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKFVGPPPERDIASLP

10015386.121201

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
 GGAGCGGGGCCCTGCAACACATGCCCCCGGGTGGGCAGGGGTGGCGCGCGCGCTGCGCGCC
 CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCTCCAGCCGTGCGCTGCC
 CACCAAGTGTACTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCTCGCGCGGTTT
 CTCGGGGATCCCCCGCAAGCTGAGCGCCTTGACCTGGACAGAAATATATCACCAGGATC
 ACCAAGATGGACTTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACAGGT
 CAGCGTCACTCAGAGAGGGCGCCTTCCAGGACCTGAGCAGCTAGAGCCACTGCGCTGAACA
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTTGAGTGAACACAGATCCAGGGGATCCGAGGAAGGCGTTCGCGCGCATCACCAGTGT
 GAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
 TGGCGGATTGGAGATCCTTACCCTCAACAACAACACATCAGTCGCATCCTGGTCACCAAGC
 TTCAACACATGCCGAAGATCCGAACCTCTGCGCTCCACTCCAACCACTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACACTT
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAAGAAGGAGTACGTG
 TGGCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAATCCATCTCTGCCCCCTGCC
 CTGACGCTGCAGCAATAACATCTGGAGCTGCGAGGAAAGGGCTTGATGGAGATTCCTGCCA
 ACTTGGCGGAGGGCATCGTCGAAATACGCTAGAACAGAACTCCATCAAGGCATCCCTGCA
 GGAGCCTTCAACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
 AGATCACCGAGATTGCCAAGGGACTGTTGATGGCTGGTGTCCCTACAGCTGCTCCATCTC
 AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCCGCCCTCTGCAGT
 CCATCCAGACACTCCACTTAGCCCAAACCCATTGTGTGCGACTGCCACTTGAAGTGGCGTG
 GCGGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCGCTGCAGCAGCCGCGCGC
 ACTGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCGAGAAGTGTGCG
 TGTGAGGCGACGATTGTGGACTGCTCAACCAAGAGCTGGTCCGCATCCCAGCCACCTCCC
 TGAATATGTACCGACCTGGGACTGAAATGACAATGAGGTATCTGTTTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCTGCGAGAGCTGATGCTGCACAGGGAACAGCT
 GGAGACCGTGCACGGGCGCGTGTTCCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACGCTTGTCTCCCT
 GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCTGGCTCGGCA
 AGTGGTTGAGGAAGAGCGGATCGTCAGTGGGAACCTTAGTGCCAGAAGCCATTTTCTCT
 AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGAT
 GCAGCAACAAGGGGCTCCGCGCCTCCCCAGAGGCATGCCAAGGATGACCGAGCTGTAC
 CTGGAAGGAAACACCTAAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTAACACTTCAGTAACATGTCTC
 ACCTCTCCACTGTATCCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCACGCCCTCAAC
 GGGCTGCGGTCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTGGAAGG
 CTCCTTCAACGACCTCAGTCTCTTTCCACTGTGGCGCTGGGAACCAACCACTCCACTGTG
 ACTGCAGTCTTCGGTGGCTGTCCGAGTGGGTGAAGGCGGGGTACAAGGAGCTTGCATCGCC
 CGCTGCAGTAGCCCTGAGGCCATGGCTGCAGCGCTCTGCTCAACCCCAACCCACCGCTT
 CCAGTGCAAGGGGCGAGTGGACATCAACATTGTGGCCAATGACATGCTGCTCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCCTGTGCTCGCCC

1005536.121201

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTGACGATG
 AGGCCAAGTGCATCCCCCTGGACAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGGCCGACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG
 AACACCCCCACCCATGGTCTACTGCAGACCAGCCCATGCGACCACTGACAGTGCAGAAC
 GGGGCCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACACAGGCTTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGAGACTCCTACGTGGAAGTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCTGCAAGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG
 GCAAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGGCCAGGGCACGG
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCGAG
 GACTTCAAGGCCCTCCACACACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCAACCGT
 GTGCAAGCAGCGGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGAAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGG
 GAGCACTGCCAACAAGAGAATCCGTGCCGTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCT
 GTGGGCCCCAGTGTGCCAGCCCACCCGACGACAAGCGGCGGAAATACGCTCTTCCAGTGCACG
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
 CTAAGCCCTTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAATGAAGCTGGAGAGGAAGGTAAAGAAGA
 AGAGAATATTAAGTATATTGTAAATAAACAATAAATAAGAACTAAAAA
 AAAAAA

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MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHLGLRAVPRGIPRN
AERLDLRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL
PELLFQSTPKLTRLDLSENQIQGIPKFAFRGITDVKNLQLDNNHISICIEDGAFRALRDLBIT
TLNNNNISRILVTSFNHMPKIRTLRLHSHNLYCDCHLAWLSDWLRQRRTVGQFTTLCMAPVHL
RGFNVADVQKKEYVCPAPHSEPPSCNANSISPCSPCTCSNNIVDCRKGKGLMEIPANLPEGIV
EIRLEQNSIKAIPAGAFTQYKKLRIDISKNIQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK
GLFDGLVLSQLLLLNNANKINCLRVNTFQDLQNLNLLSLYDNKLQITISKGLFAPLQSIQTLHL
AQNPFCVDCCHLKWLDLYLDNPIETSGARCSSPRLANKRISQIKSKKFRCSGSEDEYSRFS
SECFMDLVCPKECRCEGATIVDCSNQKLRVIPSHLPEYVTDLRLNDNEVSLEATGIFKKLPN
LRKINNNSNKIKEVREGAFDGAASVQELMGTNLQLETVHGRVFRGLSGLKTLRLNSNLISC
SNDTFAGLSVRLLSLYDNRIITTPGAFTTNVLSLTINLLSNPNCNCHLAWLKGWLRKR
IVSGNPRCQKPFPLKEIPIQDVAIQDFTCDGNEESSQLSPRCPEQCTCMTETVVRCSNKG
ALPRGMPKDVTELYEGNHLTAVPRELSALRHLLTIDLNNNSISMLTNYTFSNMSHLSTLIL
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWL
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFOCKGPVDINIVAKNACLSSPCKNNGT
CTQDPVELYRCACPYSYKGKDVTPINTCIQNPCQHGHTCHLSDSHKDGFCSCPLGFEGQR
CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVFELNLCQHEAKCIP
DKGFSCECVPGYSGKLCETDNDDCAHAKCRHGAQCVDITNGYTCTCPQGFSGPFCEHPPMV
LLQTSPCDQYECQNGAQCIIVVQQEPTCRCPGFGAGPRCEKLITVNFVGKDSYVELASAKVRP
QANISLQVATDKDNGILYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
VELVTNLNQLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCCECRPGWTGFLC
QDEARDPCLGRCHHGKQVATQCTSYMCKAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
QGEPEYCLCQPGFSGEHCVCENPCLSGQVVREIVRRQKGYASCATASKVPIMECRGGCGPQQC
PTRSKRRKYVFOCTDGSFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAAC**TGGCA**AAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGA~~AAAA~~AGGCTGTGAGGTTCC**TAA**ACTGGAAC**TGG**ACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTTCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTCC**TCC**CAATA
TTCCTTCTCAA**ACT**TGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFS LGN WICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

10015386.121201

FIGURE 115

CAGGCCATTTCATCCCCTGTCCTTGTGTTCCGAGCCAGGCCACACCGTCTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCC
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCTGTATCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCTGATGTCTCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAAGTCAATTGCTGTTAATTCGGGTGGACCTTGGAGT
 CCATTGACCAAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCTTAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTATATAATCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCAACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTATGCTATAATCATTCCAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTTGAATGATACTGTGCCCTAATTGGTTTTCATAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCAGATTCAAT
 CCACCGAAGTGTTCACTGTCTCTGTTAGGGAATTTTTGTTTGCCTGTCTTGGCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGTGTTTATCATAAAAA

1015335.121201
 1015335.121201

FIGURE 116

MPLLKL VHGSPLVFGEKFKLFTLV SACIPV FRLARRRKKILFYCHFPDLLLT KRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPD PVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

10015386.121201

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT
 CGCGGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAAGTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTTGCATGAGTTCCCTGGTTAAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTGGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTGCG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTCAC
 TTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTGCAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCATTATTATT
 CCTAGAGAGACCTCGTCCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACCAACATTTAAAA
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAAATATAAACACCTATTTGTAC
 TTAA

10013336.121204
 10013336.121204

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTV DVLKQHINPNKTS DPFETMLKSLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKSEELLDKWLSYPETQHVPLSQHMLGFMKSVTQMVMGSTFE
DDQEVIRFQKNHGT VWSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFGSTQECPELRFAYMVT TVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

10015386-124201

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTATCACCTTATTCTGGTCCCGGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTACGTTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
 TGGCCGCGCTCTCTGTCAACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCAACCGTCTTTGGGCTGAAA
 AAGAAACCCTTCTGAATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggaca
 ATTAAAAAAAAAAAAA

10015336-121201

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPITFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

10015386-121201

FIGURE 121

TCCCGGACCCCTGCCGCCCTGCCACT**ATGT**CCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCCTGCTGCAGCCCCATA
 GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
 AGCAGGCCCCGAATGTGCAGCACTACACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
 CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCACTACATGG
 ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCT**TGA**GGCC
 CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAACCCCACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

10015366.1.1201

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPERNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

10015386.121201

FIGURE 123

CTGGGACCCCGAAAAAGAGAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGTGCTGCTTCTGTTCTCGTGGTCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCATGGCCAATTCCACTCT
 CCTAGGGTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCC
 TCGTCCCCCAGTAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAAATCTTAACTGCCGATGGAGTGGGAGAAGGTAGAACGGGGCCCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCGGGGAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGGAAGGGTGTGGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTCTGAGCATG
 GCATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCATT
 GCTGATGGCACACCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGAGCCGGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGGCCGGCAGAG
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAATAAGCTT
 GCCCGGGGCA

10015386.121201

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPTYNYHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGTAGACTTTCAGATGTCTAGGAACACAGAGTGGGTGCAGGGGCCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACC GGATCCCGGGGTAGGAGGCGACGCGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACC**ATG**GGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGCTCTGGGCACAGAACGACACGGAGCC
 CATCGTGTGAGGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGGCCAGGACTCCAAGG
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGCACAA
 GAAAAGGAATTTACAGTTTCAGTTTTTACGCTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACCTGTATGTTAAATGGAACACAGTAATATCTGCCCTTTCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG
 TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCACTCCTG
 AGTTATTGGAAGATCATTTTTTATCATTTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTTCTAGCCTGTCTGAACCAATACAAAATTTTCACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTGTTTTTATTCCTTTGGAATTAGTTTGGTTTGGTTCTTGTA
 AAAACCTGGATTTTTTTTTTTCAGTAACCTGGTATTATGTTTTCTCTTAAAAAAGGTAATGAA
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACCTTTATTGC
 TCAACTTTAATTAAAAATGATTGATAATAACCACTTTATTAACCACTAAGGTTTTTTTTTTT
 TCCGTAGACATGACCACCTTTATTAAGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTGAAGTATCATCTGTTTTGCTTAACTCTTAAATTTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
 CTTGTCTTTGTATAGTCATATGAATTCATAAAATTTATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

1015335.121201

FIGURE 126

MGSGRRALSAPPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVVFVAPRKGIIYSFSF
HVIKQYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCGCTGCGCTC
GCCCTTTATGTCCTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCCTCTGTC
TATATCCAAGAAATGTTCCGATTTCATATTTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCCTTATTATGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

101535:12104

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFETIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCACCCAGCGCGCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTCTGGGCTTGCCCTTCT
 TGGTGTCTTGGTGGCTCGGTGAGAGGCCATCTGGGGGTTCTGGGGCCCAAGAAGCTCTGCGAAGAAGACGCCG
 AGTTTGAAGCGCACTACGTGGACGAGGTCAACAGCGAGTGGTCAACATCTACACCTTCAACCATCTGTGACCC
 GTACACAGGACAGAGGGCGTGGTGTCTGTGAACGTCTGAAACAGCAGAGAGGGGCGCGTGTCTGTTTGTGG
 TCCGCCAGAGAGGGCTGTGGTGTCTTCCAGGTGCCCTTAATCTCGGAGGGATGTTTACGCCGAAGTACCTCT
 ACCAAAAAGTGAACCAACCTGTGTGAGCCCCACCAAGAATGAGTCGGAGATTCAGTCTTCTACGTGGGATG
 TGTACCCCTGTACACAGTCAACACCACATACCGACTCCGGGTACGCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTCAGTCTCAATACACACAGCAGCACGCCAGTACTTCAAGTATGAGTTCCTGAAGGCGTGGACT
 CGGTAAATTGTCAAGGTGAACCTCCAACAGGCTTCCCTGCTCAGTCACTCTCAGTATGATCTCTGTGCTCTG
 TCTATGACCTGGACAACACGTAGCCTTTCATCGGCATGTACACAGCATGACCAAGAAGCGGCCATCACCGTAC
 AGCGCAAGAGACTTCCCCAGCACAGCTTTTATCTGCTGGTGTGAAGCCGAAGACCAAGCTGTGCGGGGCT
 CCGTGCCTTTTACCCCTTCGCGAGAAGATGAACCGGTGATGATCAAGGGCCTGCTGAGTGTGCTGCTGCTG
 TGTCTCAAGCAGTCAAGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGGCTGGGTATATTTTCTCTCTTTTAC
 TGCTGACCTCTCTGCTGCTGCGAGAACTGGAGGAGAGAGAACCTGCTGGTGGCCATGTACCGAG
 CCTGCCAGAAAGCGGTCACTCGAGTCTGCGTGAATCTTTTCTGGCAGTTCCTCTATGAGGGTTACAACAT
 ATGCTCTCTTTGAGAATTTCTCGGATACCGATGGTGTGGTGAACGGCTGGCATCGGGACCTCTCTTACG
 GTTACACAGGCGCGCTCTTTGAAGCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGTCTGTGGAGGAGGATG
 ACTACGACACATTGACCGCATGATTCCGACAAGAATGTATTGCAACCAAGTACCTCTATGTGGTGTGACC
 TGGCAGGCAAGGACAAGGCTTTCTGCGGAAAAAGTACAGATCTACTTCTGGAACATTGCCACCATTTGCTGTCT
 TCTATGCTCTTCTGTGGTACCTGGTGTATCACTACAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
 GCTACTACAACCTCTCTGCGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACTCTCAGCAACCTGGGT
 ACATCTCTCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCAACAGCGGCCCTGCTCGGCA
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCAACACTTTGGGCTTTTACGCCATGGGCAAGCGCTGATGA
 TGGAGGGGCTGCTCAGTCTGCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCGTTTGT
 ACATGATCGCCGAGCTGCTCATGCTGAAGCTCTACAGAAAGCGGCAACCGGACATCAACGCCAGCGCTACAGT
 CTACGCGCTGCTGGCCATTGTCTCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAGGGAAACACGCGCTTCT
 GGTCTGCTCTTCCATCATTCATCATCGCCACCTGCTCTCAGCAGCGAGCTCTATTACATGGGCGGTGGGA
 AACTGACTCGGGGATCTTCCGCGCATCTCCACGTGCTTACACAGACTGCATCCGCGAGTCAGCGGGCGC
 TCTACGTGGACCGCATGGTGTCTGTGATGGGCAACGTCTACACTGGTCTGCTGGCTGCTTATGGGCTTATCA
 TGGCGCCCAATGATTTTCGCTTCTACTTTGTTGGCCATTGGCATCTGCAAGCTGCTTTTACTTTCGCTTATCA
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCTGCTCTGATCGTTTGACACTCCGTGGTCT
 GGGGCTTCGCGCTCTTCTTCTTCTCCAGGACTCAGCACTGGCAGAAAAACCTTGCAGAGTCTGAGGAGCACA
 ACCGGGAGTGCATCTCTCGACTTCTTGACGACCAGACATCTGGCAGCTTCTCTCTCTCATGCCATGTTCTG
 GGTCTTCTGTGTTGCTGACATGGATGACGAGTGGATCTGTGACGCGACAAGATCATATGCTCTTACG
 AGGAGTCTGGGCTTCTGCTTCACTCAAGGGGCCCTGAGTCTCTTGTGTATGAGACCTGCTACTCTGTGCTGCT
 GTGGGATGAGTCCAGCACCTGCGCCAGCACTGGATGGACAGGACAGCGAGTCTGCTTAGCTTGGCTCT
 GGGACAGCCATGGGTTGGCTGGAACCTTGCAGTCTGCCCTTGGCGAGGACAGGCTGCTCCCTGGCAACCT
 AGATGTTGGCCAAATGCTTCTTCTCAGTGTGGGCGCTTCCATGGGCGCTGCTCTTGGCTCTCCATTT
 GTCCTTTGCAAGAGGAAGGATGGAAGGACACCTCCCATTTTCATGCCCTTGCATTTTGGCCGCTCTCTCC
 ACAATGCCCAAGCTGGACACCTTAAGGCTCTTTTCTCTCCCATCTCCCATCCAGGCGTAGTCTGGGGCGTGA
 ATCTCTGTCTGTATCAGGGCCCAAGTCTCTTTGGGCTGCTCCGTGCTGCTATGCTGCTGCTGCTGCTGCT
 AGATGTTGGGATGAGTATGAGATTTGGGGTGGCCAGCTGTGTCAGACTTTTGGTGTGAAGGCTGCAAGGG
 CCTGGGCGAGTGCCTATCTTCTCTGACTCAGGCTGCTCTTTAGCAATGCTGCTGCTGCTGCTGCTGCTGCT
 TGAAGAACCGCTTCTGATTCAGAGGCTGAATCAGAGGTCACTCTTATCCCATGCTGCTGCTGCTGCTGCTGCT
 AGCACAAGGACTGGAGGAGAGCGCTCACCCTTCTCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 ACTGCTGGCTCTCAGTGCATTCAGACTGCAACGAAGTTCAGGGGCAAGGAGGATGATACAGAGTTCAG
 AGTTGCTGTGTAGTATGCACACATACCTTGAACCTTGAAGTTCAGAAAGGCTTCAGGAAGGAGTGTGCTGTTT
 CCTCTAGTGTCCCGACTCTAGCTGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA
 AGTTGCTGTGTAGTATGCACACATACCTTGAACCTTGAAGTTCAGAAAGGCTTCAGGAAGGAGTGTGCTGTTT
 CCTGCGCCACTCGTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CCGGCGCTGCTGCTTGGGATGGAATGTGTTTCTCCAACTTGTGTTTATAGCTGCTGCTTGAAGGCTGGG
 AGATGAGTGGGTCTGGATCTTTCTCAGAGCTCTCCTATGCTATGGTGCATTTCCGTTTCTATGAATGAAT
 TGCATTCAATAAACACCAAGACTCAAAAAA

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FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659

><subunit 1 of 1, 832 aa, 1 stop

><MW: 94454, pI: 6.94, NX(S/T): 12

MFALGLPFLVLLVASVESHGLVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFORKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSDVI
VKVTSNKAFCPSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAATVQRKDFPSNSFYVVVV
VKTEDQACGGSPLFPYFPAEDEPVDQGHRQKTLVLSVQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLTLLVAIDRACPESGHPRLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEFVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFNWNIATIAVFYALPVVQLVITYQTVVNVGTNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPTYNTNFQDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFSIIHIIATLLSTQLYMGWRKLDGIFRRIHLVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDLDDLDTVQRDKIYVF

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

10015336.121201

FIGURE 131

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCTGTCTTG
 ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCTCCCGCAGGCTCTCCCCAAGGC
 CCAGGCTGCAGAGCTGCTGTGTGGAAGTTCCAGAAAACTATGGTGGAAATTTCCCTTTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAAGGGGACTCA
 GGCAGGCCAACTGAGGCCCATTTTGTATGGATCCAGATTCTGGCTTCTGTGTTGACCAAG
 GCCCCGTGGACCGAGAGGAGCAGGCAGAGTACCAGTACAGGTACACCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAAGCCCTGGCATCCC
 CTTCTCTTCTTGTAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAAGCCTTGACCACGCCCTGGAGAGGAC
 CTACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAACTCTCAAAGTCTTATACCCGCACCATGAGGCTGAGGCTGAGGTGGGGGTGATGT
 GCACATACCTGGAGAGCCATCCCCCGGGACCTTTGAAGTGAATGCAGAGGGGAAACCTCT
 ACGTGACCAAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGTGTGGGCTCAG
 AATTCCTTGGCAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACTGGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGACTGACCTGTACAGCAGAGGATGCAGATGCCCCGGCTCCCCAATTCC
 CACGTTGTGATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGTGTCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCACAGCACCGTGT
 GAAGTCGAAGTCGAGTACAGATATCAATGATCACGCCCTGAGTTTCATCACTTCCCAGAT
 TGGGCTTATAAGCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCTTCCGCTCATGGATTTTGGCATTGAGAGGGGAGACACA
 GAAGGCACTTTTGGCCTGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCAAGTTGGACCAGGAGCTACGAGGCCAGTGTCCCATCAGTGCCCC
 AGCCGGCTCTTTCTCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCTCCGGGAGGTGCACACC
 GCGGACTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTTCCAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGTGCTGAGTGCAGCCAGCAAGGACCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
 TTCACCTTGGTCCCAACCCACGGTGCACGGGATTGGCGCTTCCAGACTCTCAATGGTTTC
 CCATGCTTACCTACCTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTGACGCCAATGCCCCAGATGTGGCAGCTCTGTTGTTGAGATGCTGTGCTGTGCAAC
 GTGGAGGGGACGTGATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC
 AGTGGGCATCCTTGTAGGCACCTTGGTAGCAATAGGAATCTTCTCATCTCTTTCACCC
 ACTGGACCATGTCAAGGAAGGACCCGGATCAACAGCAGACGGCTGCCCTGAAGGGCG
 ACTGTCTGAATGGCCACAGCAGCTTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGACCCACGACCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCAT
 CTGCCCTGGGTGGAGGCACCATCACCATCACCAGCATGTCTGCAGAGCTGGACACCAAC
 TTTATGGAATGCCATGGGAGTGCTCCAATGTGAGGTGTTTGCCCAATAATAAAGCCCCA
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

10015386.121201

FIGURE 132

MVPAWLWLLCVSVQPALPKAQPAELSVVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDPMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDQASGHQATATVEVSIIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLEHLVLMVDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPFRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPSDGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLTTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALTLPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLTALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

10015336-121201

FIGURE 133

CCGGGGACATGAGGTGGATACGTTCATTGGGGCCCTATTGGGTCAGCATCTGTGGCCAA
 GAAAAATTTTGGGGACCAAGTTTGGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATCAAACAACCTGAAGCTCAATTTCTGGAAAACTCCCTCCTCCT
 TCAATCGGCGCTGTGGATGTCTTGGTCCCATCTGCACTGTCAGGCATTTAAACCTTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATGAGGACCTGTCAGGCCCTTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAAATTCACTACGGGG
 CTTACCATTCCCTGGAAGCTATTACCACGAGATGGACAACATTGCCGAGACTTTCTTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCTGTTGAAAACCGGCCGATGTATGTAAGT
 CAGCACTGGGAAAGCGTGAGGCGGCCGCGCTTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAAATGGATATTTCTTGTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCTTGCTCCGAAGTGACCATGGACCCACGCCAATTCGGAAGTGGGA
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGGCTGTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAAACGCGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
 TTCTCCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCGCACTGAGGCCATTGTTAAAGGAGCTCTTCTACCTGTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACCT
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC
 TGAGATGATTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACCAACTTGCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTAAATTTT
 TCGCAGTCTTCTGGAATAATTTTCCCTTTGAGCAGCAAATCTTGTAGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCCTGTTTTTTTTTTTTTTTTTTTGTAGACAGATTTTGTCTTGTGGC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCCTCTGGGTTCAAGCA
 ATTCTCTGCCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTTGTGTTTTTGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
 ACCTCAGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCGGGGCCGTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTGTGTTTGTGCTGTG
 ACCAGGATGGCGGGAGGGATCTGTGTCACTGTAGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTCAGGATGGTGAATTTATCCCATCTGCTCAATGGCTTACCTCT
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTTCCCATTTGTGCTGTGGTGTATCTGTGTT
 TCTTGTCTGGTTTG
 TCTGTCTAATTTGTATCTTGGACCACAAGTTCTAAGTAGAGCAAGAAATTCATCAACAGCT
 GCCTCTGTGTTTTCATTTTCACTCAGCAGTACCATCTGCTCTTTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAATCTTAACCTCGCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAAATGTGAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITTSILEKMDIFLLPVANPDGYVYTQTQNLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPAEETWLGKLTIMEHVRDNLV

Signal peptide:

amino acids 1-16

135/249

FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCAAAATG
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCTCTGTGCTCCAATCTACTGTGTGTC
CCCGGCCAATGCCCCAGTGATACCCCCGCCCTTCTCCACAAGAGCACCCCTGCCTCAC
AGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCATATACCGCAGGCTGGTTTTGGAGACC
CCGAGTCAGAACATCTTCTTCTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT
TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCAGC
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCAAGGGAAGGTT
GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT
TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCTGG
TGGGCGAGCAGGTCACTGTGCAAGTCCCCTGATGCACCAGAAAGAGCAGTTTCGCTTTTGGG
GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT
CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCCTTGTGAGCCAGAACAC
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCAGATTTTCC
ATTTCTGCCTCCTACAATCTGGAACCATCCTCCGAAGATGGGCATCCAAAATGCCTTTGA
CAAAAATGCTGATTTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTTCTAAGCAACCC
ACAAGGCTGTGCTGGATGTGAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCT
GATGATGATTACAATAAAGCCACAGACGGTATTCTTTCTAGGGAAAGTGGAAAATCCCA
CTAAATCCTAGTGGGAAATGGCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAA
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTGCTG
GCAGGGATGCCATTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCAGTCACAGCC
AACACCCATTAAACCCAGTCAGTGCCTTTTCCACAAATTCTCCAGGTAAGTACTGCTTCATG
GGATGTTGCTGGGTTACCATATTTCCATTCTTGGGGCTCCCAGGAATGGAATACGCCAAC
CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAATATGAAT
TCAA
AAAAAA

101536:12201

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSA LFVKKE LQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNC FVLQMDYKGD AVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNADFKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

1015336.121201

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCG
 CTGAGTCCAGATTTCTTCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAGCACCAG
 CCTTTATCTCTTACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGGCTTCCAGCCACAAAGAGACAGATGAAGATGC
 AGAAAGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCA
 CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGGCCAGCACAGTCACCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
 CTCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGTCCAGCA
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCCAGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCCAG
 TGGGGCCAAACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACAGCCAC
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTAGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACT
 TCCAGTGGGGCCAAACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACCTCCCATAGTGCATCTACTGCAGTGAAGTGGGCCAA
 AGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATACCTGGTCTCGGTGTGTGGCG
 GCCGTGGGGCTCTTTGCTGGGCTCTTCTCTGTGTGAGAAACAGCTGTCCCTGAGAAACAC
 CTTTAAACAGCTGTCTACCACCCTCATGGCTCAACCATGGCTTGGTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCTAAGTGTCTGGAGGAGACACAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGGAGGCCCGGAGACCAAG
 TGCCGCAATTCTTCAAGGAGGAGACCTGGGCACCAAGACCTGGTTTCCTTTCATTTCATC
 CCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAAATCTTTGAAGAAGGTATTCTCACC
 TTTCTTGCCCTTACAGACACTGGAAGAGAAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCGGGGTGGGTATCTAG
 CTCTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAATCCAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAA

10015386-121201

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSSVISSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSIVTNSEFHMTSSSGISTATNSEFSTASSGISIATNESSTSSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSS
 TTSSGASTATNESSTSSGASTATNESSTVSSRASTATNESSTSSGASTATNESRTT
 SNGAGTATNESSTSSGASTATNSDSSTVSSGASTATNESSTSSGASTATNESSTSS
 GASTATNSDSSSTSSGAGTATNESSTVSSGISTVTNESSTPSSGANTATNESSTSSGA
 NTATNESSTVSSGASTATNESSTSSGVSTATNESSTSSGASTATNSDSSSTSSEAST
 ATNESSTVSSGISTVTNESSTSSGANTATNSGSSVTSAGSGTAALTMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAGLFFAGLFFCVRNSLSLRNTFNTAVYHHPGLNHGLGP
 GPGGNHGAPHRRPWPSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

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FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTTAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
 GGATTTGTGAATAAACTTGATACACCA

10111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001301130213031304130513061307130813091310131113121313131413151316131713181319132013211322132313241325132613271328132913301331133213331334133513361337133813391340134113421343134413451346134713481349135013511352135313541355135613571358135913601361136213631364136513661367136813691370137113721373137413751376137713781379138013811382138313841385138613871388138913901391139213931394139513961397139813991400140114021403140414051406140714081409141014111412141314141415141614171418141914201421142214231424142514261427142814291430143114321433143414351436143714381439144014411442144314441445144614471448144914501451145214531454145514561457145814591460146114621463146414651466146714681469147014711472147314741475147614771478147914801481148214831484148514861487148814891490149114921493149414951496149714981499150015011502150315041505150615071508150915101511151215131514151515161517151815191520152115221523152415251526152715281529153015311532153315341535153615371538153915401541154215431544154515461547154815491550155115521553155415551556155715581559156015611562156315641565156615671568156915701571157215731574157515761577157815791580158115821583158415851586158715881589159015911592159315941595159615971598159916001601160216031604160516061607160816091610161116121613161416151616161716181619162016211622162316241625162616271628162916301631163216331634163516361637163816391640164116421643164416451646164716481649165016511652165316541655165616571658165916601661166216631664166516661667166816691670167116721673167416751676167716781679168016811682168316841685168616871688168916901691169216931694169516961697169816991700170117021703170417051706170717081709171017111712171317141715171617171718171917201721172217231724172517261727172817291730173117321733173417351736173717381739174017411742174317441745174617471748174917501751175217531754175517561757175817591760176117621763176417651766176717681769177017711772177317741775177617771778177917801781178217831784178517861787178817891790179117921793179417951796179717981799180018011802180318041805180618071808180918101811181218131814181518161817181818191820182118221823182418251826182718281829183018311832183318341835183618371838183918401841184218431844184518461847184818491850185118521853185418551856185718581859186018611862186318641865186618671868186918701871187218731874187518761877187818791880188118821883188418851886188718881889189018911892189318941895189618971898189919001901190219031904190519061907190819091910191119121913191419151916191719181919192019211922192319241925192619271928192919301931193219331934193519361937193819391940194119421943194419451946194719481949195019511952195319541955195619571958195919601961196219631964196519661967196819691970197119721973197419751976197719781979198019811982198319841985198619871988198919901991199219931994199519961997199819992000200120022003200420052006200720082009201020112012201320142015201620172018201920202021202220232024202520262027202820292030203120322033203420352036203720382039204020412042204320442045204620472048204920502051205220532054205520562057205820592060206120622063206420652066206720682069207020712072207320742075207620772078207920802081208220832084208520862087208820892090209120922093209420952096209720982099210021012102210321042105210621072108210921102111211221132114211521162117211821192120212121222123212421252126212721282129213021312132213321342135213621372138213921402141214221432144214521462147214821492150215121522153215421552156215721582159216021612162216321642165216621672168216921702171217221732174217521762177217821792180218121822183218421852186218721882189219021912192219321942195219621972198219922002201220222032204220522062207220822092210221122122213221422152216221722182219222022212222222322242225222622272228222922302231223222332234223522362237223822392240224122422243224422452246224722482249225022512252225322542255225622572258225922602261226222632264226522662267226822692270227122722273227422752276227722782279228022812282228322842285228622872288228922902291229222932294229522962297229822992300230123022303230423052306230723082309231023112312231323142315231623172318231923202321232223232324232523262327232823292330233123322333233423352336233723382339234023412342234323442345234623472348234923502351235223532354235523562357235823592360236123622363236423652366236723682369237023712372237323742375237623772378237923802381238223832384238523862387238823892390239123922393239423952396239723982399240024012402240324042405240624072408240924102411241224132414241524162417241824192420242124222423242424252426242724282429243024312432243324342435243624372438243924402441244224432444244524462447244824492450245124522453245424552456245724582459246024612462246324642465246624672468246924702471247224732474247524762477247824792480248124822483248424852486248724882489249024912492249324942495249624972498249925002501250225032504250525062507250825092510251125122513251425152516251725182519252025212522252325242525252625272528252925302531253225332534253525362537253825392540254125422543254425452546254725482549255025512552255325542555255625572558255925602561256225632564256525662567256825692570257125722573257425752576257725782579258025812582258325842585258625872588258925902591259225932594259525962597259825992600260126022603260426052606260726082609261026112612261326142615261626172618261926202621262226232624262526262627262826292630263126322633263426352636263726382639264026412642264326442645264626472648264926502651265226532654265526562657265826592660266126622663266426652666266726682669267026712672267326742675267626772678267926802681268226832684268526862687268826892690269126922693269426952696269726982699270027012702270327042705270627072708270927102711271227132714271527162717271827192720272127222723272427252726272727282729273027312732273327342735273627372738273927402741274227432744274527462747274827492750275127522753275427552756275727582759276027612762276327642765276627672768276927702771277227732774277527762777277827792780278127822783278427852786278727882789279027912792279327942795279627972798279928002801280228032804280528062807280828092810281128122813281428152816281728182819282028212822282328242825282628272828282928302831283228332834283528362837283828392840284128422843284428452846284728482849285028512852285328542855285628572858285928602861286228632864286528662867286828692870287128722873287428752876287728782879288028812882288328842885288628872888288928902891289228932894289528962897289828992900290129022903290429052906290729082909291029112912291329142915291629172918291929202921292229232924292529262927292829292930293129322933293429352936293729382939294029412942294329442945294629472948294929502951295229532954295529562957295829592960296129622963296429652966296729682969297029712972297329742975297629772978297929802981298229832984298529862987298829892990299129922993299429952996299729982999300030013002300330043005300630073008300930103011301230133014301530163017301830193020302130223023302430253026302730283029303030313032303330343035303630373038303930403041304230433044304530463047304830493050305130523053305430553056305730583059306030613062306330643065306630673068306930703071307230733074307530763077307830793080308130823083308430853086308730883089309030913092309330943095309630973098309931003101310231033104310531063107310831093110311131123113311431153116311731183119312031213122312331243125312631273128312931303131313231333134313531363137313831393140314131423143314431453146314731483149315031513152315331543155315631573158315931603161316231633164316531663167316831693170317131723173317431753176317731783179318031813182318331843185318631873188318931903191319231933194319531

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

1015336 121201
102121 9855001

FIGURE 141

CTCCGGTCCCCAGGGGCTGCGCCGGGCCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGCGGGGGCGATGACCGTGCGCTGACCCCTGACTCACTCCAGGTCCGGAGCGGGGGCCCCCGGGGCGACTCG
 GGGGCGGACCGCGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACTGAGCCCCAGGCGGGGACACCGTCT
 GCTCCTGCTCTCCGAATGCTGCGCACCGGATGGGCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGTGGCCG
 CCTCGGCCACGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGAGCCGCCGCTCCGACCTGGGGCGCTCAGC
 CCCCGGATCAGCCTGCTCTGGGCTCTGAAGAGCGGGCCATTCCTCAGATTGGAAGCTGAACACATCTCCAACATC
 ACAGCCCTTCTGCTGAGCAGGATGGCAGGACCTGTACGTGGGTCTCGAGAGGCCCTTTTGACTCAGTAGC
 AACCTCAGTCTCTGCGCAGGCGGGGATACCAGGAGCTGCTTTGGGCTGCAGACCGCAGAGAGAAACACAGCTGC
 AGCTTCAAGGGCAAGGATGCTCCTCTGCAAGATGGCAGCGACTGTCAAACTACATCAAGATCCTCTGCCGTACGGGCGAGTCA
 CTGTTCACTGTGGCAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGAGAACTTCCACTGGCAGG
 GACGAGAAGGGGAATGCTCCTCTGCAAGATGGCAGGGCCGTTGTCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGCCATCTCGCGGAGC
 CAAGCCTTCGCCCCACCAAGACCAGAGCTCCCTCAACTGGCTGCAAGACCAGCTTTTGTGGCCTCAGCCTAC
 ATTCCTGAGAGCCTGGGCAGCTTGCAGGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTGAGTCTTTGAGAACACCTTGTGTCGCCCATGCGCCGATTCGAAGGGCGATGAGGTGGAGAGCGGGGT
 CTACAGCCTGCGTGGACCTCTGCTCAAGGCCAGCTGCTGCTCACGGCCGACGATGGCTTCCCTTCAAC
 GTCTGTCAGGATGCTTCAGCTGAGGCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGTCTTCACT
 TCCAGTGGCAGAGGGGAACACAGAGGCTCTGCCGTCTGTCTTCAACATGAAGAGTGTGACAGAGTCTTC
 AGCGCGCTCTACAAGGAGCTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCGGTGCCACACCCCGG
 CTTGAGAGCTCTCATGACCAAGTGGCCGGGAAGGAAGATCAACTCATCCTGTCAGCTCCGACACCGCGTGTG
 AACTTCTCAAGGACCACTTCTGATGGAAGGCGAGTCCGAAGCCGATGCTGCTGTGAGCCCCAGCTGCGT
 TACACGCGGTGGCTGACACCGCTCCCTGGCTGACACACACTACGATGCTCTTCTGGGCACTGGTGAC
 GGGCGGCTCCCAAGGAGTGAAGCGTGGGCCCCCGGGTGACATCATTTAGGAGCTGCAGATCTTCTCATGGGA
 CAGCCGCTGCAGAACTCTCTCTGGACACCCACAGGGGCTGCTGTATGCGGCTCACACTCGGGCGTAGTCCAG
 GTGCCATGGCCAACTGCAGCTGTACCGGAGCTGGGGACTGCTCCTCGCCCGGAGCCCTCTAGTGTCTGG
 AGCGCTCCAGCTGCAAGCAGCTAGCCCTTACCAGCTCAGCTGGCCACGAGGCGGTGGATCCAGCACTCGAG
 GGAGCCAGCGCCAGGACCTTTGAGCGCGTCTTCGGTTGTGTCGCCGTCTTTGTACCAACAGGGGAGAAGCCA
 TTGTAGCAAGTCCAGTTCCAGCCAAACACAGTGAACACTTTGGCGTGGCGCTCCTCTCAACTGGCAGCCGAC
 CTCTGGCTACGCAACGGGCCCCGTCAATGCTCGGCTCCTGCGAGTGTACCCACTGGGAGCTGCTGCTG
 GTGGCACCCCAACACTGGGGAGTTCCAGTGTGTTCACTAGAGGAGGGCTTCAGCAGCTGCTAGGCCAGCTAC
 TGCCAGAGGTGGTGGAGGACGGGTGGCAGACCAACAGATGAGGTGGCAGTGTACCCGATCATTTATCAGACA
 TCGCGTGTGAGTGCACAGCTGCTGGTGGCAAGGCCAGCTGGGGTGACAGACAGCTTCTGGAAGGACTTCTGCTG
 ATGTGACAGCTCTTTGTGCTGGCGTGTGCTCCAGTTTTATTCTTGCTCTACCGGACCCGGAACAGCATGAAA
 GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGCAACCCAGACCTGCCCTGTGCTGCTGCCCCCTGAGCCCGCG
 CCACTCAAGCGCTAGGGCCCCCTAGCAGCCCCGCTCGATCACCAGGGTACAGTCCCTGTGACAGACCCCGG
 GGGGCGGAGCTTCTGCTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGCAGCTTCTGAGGAGTATCCCCAGT
 TGCCCCCGGCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGGAGCTTCCAGAGGACG
 TGCCCTGGCTTCAGGGCTGTGAATGCTCGGAGGAGCTCACTGGACCTCCCTCCGCTCTGCTCTCTGTGGAA
 ACAGCCGCTGGTGGCCGCCCTTGGAGCCTTGGAGCCAGCTGGCTGCTGCTCTGCTCAGTCAAGTAGCGGAAGCTC
 TACCACCCAGACACCCAAACAGCCGTGCCGCCAGAGTCTGGCCAAATATGGGGGCTCGCTAGGTGTGGTGA
 CAGTGTCTTATGTAACTGAGCCCTTTGTTTAAAAAACAATTCCAAATGTGAACATGAGAGGAGAGAG
 ATAGCACTGGCATGCACACACCGCTGCTCCAGTCTATGGCCCTCCAGGGGTGCTGGGAGTGCATCCAAAGTGG
 TTGCTGTGACAGCAGTGGAAACCTCACCAGCTGCCCTCTTCACTTCCAGATTAATCCCGTCCACAGGCTGCT
 CTGTCTCACTCAGATTCAAGCAGCTTGGGCTGCGTGGCTTCTGCTTGGCAGTCAGCCGAGGATGTAGTTG
 TGTGTCGCTGCTGCCACCACTCAGGACAGAGGGCTAGTTGGCACTGGCGGCTCAGCAGCTCTCGGCTG
 GGACCACTCTTGGACCTTTCCAGCTGTATCAGGCTGTGGCCACACAGAGGAGCAGCGGAGCTCAGAGAGA
 TTTCTGTCAGAACTGACGCTTTTCTCAGAACTCAGGGAAGAGACTGTGCGCTGCCCTTCTCCGTTGTCGTFGA
 GAACCGGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTTGAACCTCAACACAGGAGAACTAAGTCAAC
 CTGCTCTCTCCCGAGTCCGAGTCACTCCCTCCATCCCTCACTCTCCCATCTAAGGAGATCAACACTGCC
 AGCAGAGGGGCTCGAATTTATGTGTTTTATACATTTTTTATAGATGCATTTATGTCACTTTTTTATAA
 GTCTGAAGAACTACTGTTTAAAAAATAA

1005386.121201

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFFSETGQEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHFPVTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGHHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSlyQP
QLATRPWIQDIEGASAKDLCSASSVVSFVPTGEKPCQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPDGLLLVGTQQLGEFQCSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

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Transmembrane domains:

amino acids 23-46 (type II), 718-738

100536.121201

CTAACCGGAGGATGTGACGCTGCGCGCGCGCGCGGCTACGAAGAGGACGGGGACAGGCCCGCTGCAACCA
CGCCAGCCAGCGGAGGACGCGGCGAGGAGGACGCGGAGCGCCGAGCTGTCGCCCGCGCGCTGTCGCGCTGC
TCCGCGCGCCGCGTCCC GCGCGGAGCGGAGGAGGAGCGCGCCAGCTCGCCCGAGCGCGCTGACGCGCGCG
CGGCGAGTGGTCCCTCTTTAAAGCGCAGCGCGCGCGCGCGCGGGTGTGCGGAACAAAGCGCGCGCGCGGG
CTCGCGGCGCGTGGGGCGCGGATGATGGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCTGC
CGCGCTTAGGGCGCGCTGCCCTCGCTGGCGGGGCGAGCGGGCTTAGGGCGCGCGGAGCTCGCGCGCGCGCGCG
GCGCGCGCGCGCGCGCGCGCGCGGAGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCTGGCTACGCTGC
TGCTCGGGCTCGTCTGGGCTCTCGCTGCTGCGCTCGCGGCTGCTCGCGCGCGCTTCCGAGCTGCAAGCGAGCG
GCCACGCGCGCGCGCGACGCCCGAGGGCTGCGGCTCGGGCAGCGCGCGCTTCCAGCGCGCGCGCGCGCGCG
GCGATCGCGCGCGCGCGCGAGCTGTGGCGCGCGCTCGGACCGAGTGGCGCGCGCGCGGACAGGAACTTCTCT
TCGTGGGAGTCATAGCCGCGAGAAATCTTCGACAGTGGCGCGCGCGCGCGCGCTTCCAGAGTGTGCGCAACAGG
TCTCTGGGAAAGTTCAGTTCTTCTACAGTAGGGTTCTGACAGACTCTGTACCAATTCAGTGTGCGCAACAGG
GTGTGGAGACGCTCTACCGCGCCAGAGAAAGTCCTCATGATGCTCAGTAGTGTGACAGCACTACTTGGAGCA
AGTATGAATGGTTATGAGAGCAGATGATACGTTGTACATCAAAAGAGACGCTGTGGAGAGTTCTTGAGGAGT
TGACAGCAGCGAGCCCTCTTTCTTGGCAGCAGCGCTGGGACCGAGGAAAGTGGAAATAGGCAATGGCCCTGC
AGCCTGCTGAGAACTTCTGACATGGGGGGCGTGGGTGATCATGAGCGGAGGTGCTGTGGAGAATGGCGCGC
ACATTGGCAAGTCTCTCGGAGAGTGTACACCACCATGAGGACGTGGAGGTGGAGAGGTGTGCTCGGAGGTGTG
CAGGGGTGCAGTGTCTGTGCTTTATAGATGTGGCGAGCTTTTATGAGATACAGCAGACAAACAAAGGGGT
ACATTAGAGATCTCTTAACAGATAAATTCACCAAGTATACATATACACCCAAACAAACCCACCTACAGT
ACAGGCTCCACAGCTACATGCTGACGCCAAGATATTCGAGCTCGCCATGCGACATACAGTGCACCGCGAA
TTGTCTGTGATGAGCAATACAGCAACACAGAAATCTATAAGAGGACCTTCAGCTGGGAATCCCTCCCTCTTCA
TGAGGTTCTGACCCCGCGGACGAGGAGATCTCTGGAATGGGAGTTCTGACTGGAAATTAATGTATTGGCAG
TGTGCGGCGACCCCTCTGAAGAGGAATGAGCTGCGCGCAGAGGAGGCTTGGAGCAGATTCTATGACGTTCA
TGGAGATCATGAATGCCAACGCCAGCAGAGGCGGCGATGACTGACTCAAAGAGTCCAGTAGCGCTACGCC
GGGTGAACCCCTGATGTGGGCTGAGTACGCTCTGGACCTGCTGCTTGTACAAAAAGCAACAAAGGAGCAAAA
TGACGTCCTGTGGAGGAGCAGCGTATTTACAGCAGACTTCGTCACAAATCAGTTTCTGGAGCTATGACAGC
TGGATGCAACAGAGTTGGCCAGAGAAATCAATCAGGAATCTGGATGCTTCTGCTTCTCTCAAAATCCCTGAAG
ACGTCGTCCCTTTTACGCTCTGGGTGCGAAGATGAGCAACAAGAACCCAAAGATAAAAGTAAACATCTGA
TCTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGAAATTTTGAAGAAGCTGTCTTATCCCAAT
AGAACTCAGCTGTGGTGTCTGCTTTCAATCTGACTGCCAACCTGACAGGCGCAAAACAGTTGTAACTGTGTA
GAGATTACCGCATTAAGTCAATCGAAGCGAGCTACGAGATTGTGCTGTGTCTGGAGAGTTTTCAGAGCGCTGG
CCCTGGAATAGGATCTCCAGTTTAACTAGATTTGCTCTTCTGTGACGCTGACCTGCTGTGTTTACTA
CAGAAATCTCTTCAGGATGTGCGACAAATACATCTCGGCGCAAAATATTTTCAACATCTCTTCAGGAGT
ATGACCAAAAGATTATTATAGTGGAAAGTTCCAGCTGACACCAATTTTGCTTCTATCAAGAAATCGGCTCT
GGACAAGTATCGGTTTGGCATCAGCTGATTTTAAAGGAGACTTGTGCGAGGTGGTGGCTTTGATTTTCCA
TCCAAGCTGGGGCGGGAGTGTGACCTTTTCAACAGAGCTTGTCCAGGACAGTTTGAAGACGTTTAGGAGC
AGGAAGTAGGAGTATGCTCACTCCACATCTGCTCTTTGTGATCCCATTTTGACCCACAGCTACAAATGT
GCTTGGGGTCCAAGACATGACCTATGGGTCCACCCAGACCTGGCTGAGATGTGGCTGGAAAGAAATGATCCCA
GTACAGTAAGAGCAGCAATAATATGGCTCAGTGAAGCAGCGCTTGTGCTGACGTTCTGGAAAGACGTTT
TAATTAATTAATTTATTTTCAAAAATTTTGTATGATCAGTTTGTGAAGTCGATACAGGATATTTTAC
AAGTGGTTTCTTACATAGGACTCTTATAGATTGAGCTTTTGACACAGAGGTGATGATGTTTGCCTTTGAC
ACATCTCTCTGCTGACATATTATGACGACAGCTGCTTAACCTTTGACTTGAATGTACCTGTATGAACAAACTT
TTTAAAAAATGTTTCTTTTGGAGCGCTTGTCTCGACTCTATGGCGAGAAAGTCACTGTATCCCAAGTAT
TATTGTACAAACACATGTAACCTCGTGAATGTTCTGTGTAATGTAACTTCCAGATTTCTACCTTTTGT
GTTTGTGTTTTTTTTTCAATGTTTTTAAAGCAATTTGATGTCCAGTTGTAGATAGGAATGTGATATA
GCTGTTTCATCATTTCTCTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGTTACTCTGTCAGCAATGGC
CAGTAGGTTTGTGTTGTTTCTTTGTTGTTCTTTTGGAGACGAGGTCACTCTGTGTACCCAGCGTGAAGT
CAGTGGCGCAATCTGGCTCATCTTAACCTCACTTCCGCTGTACGAATTCCTCCCTGCTTGTGCTCCGAGT
ACGTGGATACAGGCAACACACCGACGCCAGCTAGTTTTTTCTATTTTATGAGAGCGGCTTACCAT
GCAAGCCAGCTGCGCAGCTAGTTTAAAGCAGGCGCGTGAAGAGGCAAGTGAAGTATGTGGCTGTCTCG
TGAGTTAGTCTGCGCTAAATAGACCTGCATTAATTTTTCAGAGAGTATGGCATTTCTCTTCTGACCTCT
GTCTTTAAAGGGTAAATATTAATCTTTAGAAATGCAACAGATGAATTAACATAAATCTGATGATACAGACT
CAACATACACACATACACCTTAACCAATGGGGAAGAAATGTAATGGTTTGTGCTCTTCACTCTGTCTG
TGTATTCTGTTGGTGGAGATGTTTTCATCTCTTCAATCACTGTTTGTATTCTTGTATCTGAATACCTTTAA
TTTTATTAAATATCTGTTTGCAGAGCTGCACATTTCTGATACCTGTTAGTTAGTATTTATGTGATTCGG
GAGTGTGTTTAGTCTGTTTATTCAGTAACCAAGCTTCCAAGAGTTTCTTTTGGAAAGCGTTTTCCTCCCT

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACAGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAACCAAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAAACACGAAAAA

1001536-121201

FIGURE 144

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
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><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWP PGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG
SDTSVIPVIVPLRGVDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPEGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKGYIRDLSHNSKIHQAITLHPKNKFP
YQYRLHSYMLSRKISLHRHTIQLHREIVLMSKYSNTEHKEDELQLGTPPSFMRFPQPRQREE
ILEWEFLTGYKLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGIIDFKELIQY
INRNENPMYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
IINSEGSLSVLSLNSKLVNPPQLPGSKSEHKPEPKDKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLFLNSLSDPNPKAQVELMRDRIYIKPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDKPKVYSGKVPDNHFAFT
QKTGFWRNYGFGITCIYKGLDVRVGGFDVSIQGWGLEVDVLFNKVQAGLTKFRSQEVGVVH
VHPVFCDPNLDPKQYKMLGSKASTYGSTQQLAEMWLEKNDPYSYKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCAGCCTGGTGCCCCAGGACGTTCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA
CAAGTTTATAGAGAACCTAGTACGAAGTGTTCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
TAATCTCCAAAACATGTTTATCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCCAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAACCTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCAGAGAGTTGGAATAAT
GATGACATTTTGAATAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAACAATAATATAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
TTTAAGCAAACGCAATTTTTCACAGGAGAAATAATCATATTGTAATTTCAAAGTTGTAT
AAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAATAAATTTTGGTTCAGGAAAAAA

FIGURE 146

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEFPYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

10015336.24201

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCCTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAAGTGAAGTGTGTAAGGACTCCATTGCAGGGGGCGTGTCTCTCTAAGGC
 TAAAAAATCATCTCCCTCGGACATCGGCCCTGTATGGGTGCTGGTTTCAGTTCACAGATTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGTATGTATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACICGGGTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTCAAATCCAAAGGAAAAATCCA
 GGGCGAATCGGACTGGAGAAGAAAGCAGGACAGGCAAGATTGAGAGCGCCCCGGAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAAATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTTAC
 ATTTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCC
 TGGACIATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAGTTTGAAGGCTTGTGTGAGACCCATATATCCAGCATGCGATGTATGACGA
 GGAAGAGGGGACTCCCATATTTCATATGTCCAGTGTCTTGGGGATGAGACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCAGACACAGCCAAGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTCTTCTGCCCCGTGAGCCCTGACAGCAGCGGAGTACAGCTTCCAGATGAGGGGGGAT
 TGGCCTGACCCTGTGGGAGTCAAGCCATGGCTGCCCTGAAGTGGGAGCGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTGTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATATGCTTGCAGGTTTGAGGGCACAGTGTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTTATCCACATTAATTTACTTTTCTCTA
 TACCAATCACCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTCTACTGATTCTATAAGCCAGCATTACCTGATACCAAAACCAGGCAAG
 AAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTAACAAATTAACATAAACAATATATTAAAGATGATATATACTACT
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATTTAAATTAACACAGTGAAT
 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

10015336.121201

FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACGTACAA
 TTACTATAGCACATTGTCAATTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCTACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTCTACTGTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCTTTGGAGTAACAATAAAACCTTCGAAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGCTGGCTGCCCT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTGTTCTCTAGAAGTTTTGTGAGAAATTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTCAGTCCCTC
 AGCTCCTCTCATTTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGGCCAAGATATA
 TCCTTATTTTCATTTCCAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGACAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAATAATCACCCA

100536.12261

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKTKYNYSTLSFTTD
KLYAEFGREASNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYPYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIYWLAGIVSWGDECAKPNKPGVYTRVLTALRDWITSKTGI
```

amino acids 21-40 (type II)

GTCTGAAGGTTATAAAGCTCTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTTGGGGATCCCTCAGCCTAACACCCACAGACGTACAGTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCTTTGCGGCTGTCCCTGCGACTACGACCACTGC
CGACACTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGGCCGCGCAGTGGTCCACTGGTGTGCCCTTCTCCCGGCTCCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATGTGCTTTGCGTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGACAGCCGCTTGGCGTGCCGCCAACCCCCGCATCTGGTCCACGC
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCGCCGAGCCGACGGGGCGCTCTGA
AAGGGGCTTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAGAGGCAAAACCCGCTGCCTCCAGGAGGCGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGTTTCTCAGGACTAGACGCTGTGTTTAGGTCGGGTACTT
GGCCCTTTGTTTCTTGCTGAGGTTCTGGGAAGGAATAGACAGGGGCCCCCAATTTTTTTTAA
AGCGGCCAGATAATAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRRAAARAAGAL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGCGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCGCATGAGCCCCCGCGTGCCTCCCCACTATCCCCAGGCGGGCTGGGGCACCCGG
 CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGGC
 TTCTCCCTTACGGGGCTCAC**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCCGTGCCTGCT
 CTACGCCCCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATTGCTGTTTGCCTGTTTCCCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
 GAACTTATGGTTCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTTAGAGAAATCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAAATGTATTCCTTTTTGAGAGGAACCAACAACCTGC
 AGGTGCTGAGGTTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAAATGATGTC
 CTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAACTCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTA**TAA**AAAGAAATGTGCAGAGAAGAAACCACAAACTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACATATGTGTTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAAAACA
 CCTAAGCATATACTATTCTATGCTTTAAATAGGATGGAAAGTTTCATGTCTATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAAATTATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACCTAAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAA
 TCTGTATAATTCAAGTCGATTTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAGGAAA
 ATTTGTCCTGTATAGCATCATATTTTTTAGCCTTTCCCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCCTAAATTTTGAAAAATA
 CCAGTGTGATACATAGGAATCATTATTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAATAA
 GAAATTTGCACATAAATCTTGTGATTCAGAAAGGACTTGTATGCTGCTTTTCTCCCAATG
 AAGACTCTTTTTGACACTAAACACTTTTTAAAGGCTTATCTTTGCGCTTCTCCAACAAGAA
 GCAATAGTCTCCAAGTCAATATAAAATCTACAGAAAAATAGTGTCTTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACCATGTGACAATTAGAGATTTCTTTTATTTCCTGATTATTA
 ATATACTGTGGCAAAATACACAGATTATAAATTTTTTACAAGAGTATAGTATATTTATTT
 GAAATGGGAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTATTCTCAGAATATGGAA
 AGAAATTAATGTGTCAATAAATATTTCTAGAGAGTAA

10015386-121201

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAE TRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSL LVI FCVELACGVWTYEQELMVPVQ
WSDMVT LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREP GTDQMMSLKN DNSQHLSCPSVELLKPSLSRI FEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

156/249

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTAGGGGACCAAGGCCGTGCC
 TGCACCTCGGGCCTCCTCCAGCCAGTGTCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATGT**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
 TGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCCACTGCAGGTGCTGG
 ACTCGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTGTGTGAATCACAGAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGTGCAGGAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAGATCATCATTCATTGAATTCACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTCTCAGGCCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCACTCCA
 GGTCATTGACAGCACCGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTGTCAGTGTGGGAGCCGCTTCCTTCTCTG
 CCCTGCCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCTGCCCCACAGCCTCAGCATTCTTTGGAGCAGCAAGGGGCTCAATTCTGTAAAGAGACCC
 TCGCAGCCCGAGAGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGCTCTGCGCCAGCCCTGTCCGTCTTCAACCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCATGCCCCACTGTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAAA

10015386.121201

FIGURE 156

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVILDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPGCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWFPQVSIQYDKQHVCVGGSSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPLAVAKIIIIIEFNPMYPKDNIDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFQKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDGGPLMYQSDQWHVVGVIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

10211336121201

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGCAGCGGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGCTGTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCTGGACCCTGGAGCCTCCTGGGGC
TTTTCCTCTTCCAACCTGCTTCAGCTGCTGTGCGGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCA
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGGGAAATACCTCTACGTGGGGGCTCGAAGAAGCCATTCTGGCCTTGGATATCCAG
ATCCAGGGGTCGCCAGGCTAAAGAACATGATACCGTGGCGCAGCACTGACAGAAAAAGAGTGAATGGCCTTTA
AGAAGAAGAGCAATGAGACACAGTGTTCACACTTCATCCGTGTCTGGTTTCTTACAATGTCAACCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTGTGACCTTCATTGAACCTTCAAGATTCTCACTGTTGCCCATCTCGG
AGGACAAGTTCATGGAGGGAAGGCCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACCTTCTGGGCACTGAGCCCATCTGATGCGCACACTGGGATCCCAGC
CTGTCTCCTAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCTCCTTTTGGGAGCCATCCTTCGACCC
AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGAATGACGTGGCGGGCGAAAGCTGCTGCAAGAAGAAGTGACACCTTCTCTGAAGGCCGACG
TGCTCTGACCCGACCGGGGAGCTGCCCTTCAAGCTCATCCGCCACGCGGTCTGTCTCCCGCCGATTCTCCCA
CAGCTCCCCACATCTACGCAGTCTTCACTCCAGTGGCAGGTTGGCGGACGAGAGCTCTGCGGTTGTGCTCT
TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAATAACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTGTCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCT
TCATGAAGGACCATTTCTTGATGGATGAGCAAGTGGTGGGGACGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA
CACGGCTTGAGTGGAGACGCCCGAGGCCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCAACAG
GGTCGCTCCACAGGCTGTGGTAAGTGGGACAGCAGTGTCTATCTGTTGAAGAGATTAGCTGTTCCCTGACC
CTGAACCTGTTCGCAACCTGACAGCTGGCCCCACCCAGGGTGAGTGTGTGAGGCTTCAGAGAGTGTCTGGA
GGGTGCCCGGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCTGGCGGACCCCACTGTGCT
GGGACCTGTAGTCCGAACCTGTTGCCCTCTGTCTGCCCCCAACTGAACCTCTGGAAGCAGGACATGGAGCGGG
GGAACCCAGAGTGGCATGTGCCAGTGGCCCCATGACAGGAGCCCTCGGCCCTCAGAGCGGCCCGCAATCATTA
AAGAAGTCTGGCTGTCCCAACTCCATCCTGGAGCTCCCTGCCCCACCTGTGAGCCTTGGCTCTTATTATT
GGAGTCATGCGCCAGCAGCAGTCCAGAAAGCCTCTTCACTGTCTACAATGGCTCCCTCTGTCTGATAGTGCAGG
ATGGAGTTGGGGTCTCTACCACTGCTGGGCACTGAGAATGGCTTTTCATACCTGTGATCTCTACTGGGTGG
ACAGCCAGGACCCAGACCTTGCCCTCGATCTGAACCTGGCAGGCATCCCGCGGAGCATGTGAAGTCCCGTTGA
CCAGGGTCAGTGTGGGGCGCCCTGGCTGCCAGCAGTCTTACTTGCCCCACTTTGTACTGTCACTGTCTCT
TTGCCTTAGTGCTTTCAGAGCCCTCATCATCTCTGTGGCTCCCACTTGAAGACACTCGGGCTCGGGGCAAGG
TTCAGGGCTGTGAGACCTTGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGAGAGCACTCTGCAGTGTGAGCAGCTGACAACACTGCTAGGCACTGAGTAGCTTAAACTCTAGGCA
CAGGCGGGGCTCGGCTGACGACCTGGCCATGCTGGCTGGGCGGCCAAGCAGACCCCTGACTAGATGACAG
CAGCAGAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCTCCCTATAGGACTCCCTTCAACAGCAGATGAGCTCTTAACAGGGTGGGGCTAC
CCCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGATCTTCACTTCTGGCCATTCCAGGGACCCCT
CAGAAACACAGTGTTTCAAGAGACCTAAAAAACCTGCGCTGCCAGGACCTATGTTAATGAACACCAACATC
TAAACAATCATATGCTAACATGCCACTCTGGAACCTCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
TCTCCAGGGTCACTGAGGGATGTGCTCCCTCCTGCTTCCCTTACAGTGTGACCGCTGACTCCAGGAAGTC
TTTCCTGAAGTCTGACCACCTTCTCTTGTCTCAGTGGGGCAGACTGTATCCCTTCTGCCCTGGCAGGAATGG
CAGGGGTAACTCTGAGCCTTCTTCACTCCTTTACCTGCTGACCCCTTCACTCTCCCTCCCTTTCTCTTGT
TTTGGGATTCAGAAAACTGCTGTGCAGAGACTGTTATTTTATTAAAAATAAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
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```
><subunit 1 of 1, 761 aa, 1 stop
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><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDNGLTYVGAREAILALDIQDPGVPRLKNMI PWPASDRKKSECAFKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPSTQVYVFFFE
ETASEFDDFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKGHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLHKAVVSGDSSAHLVEEIQLPFDPPEPVRNLQLAPTQGA VFVGFGSGGVWRVPRAN
CSVYESCDVCLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQWATENGFSYPVISYVWDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFAVNLGSAIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASVDADPNCLNGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
 TGAGCATGCTGGGCAGCGAGTGTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTGTCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACATGCTTAACCAAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAGAGAAATTTAAAAAGAGTTTGATTCTTTCTGGAAGAAACTTTAGG
 TGGCAGAGGAAAAATTTGAAAACCTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAGAATGAGAATTCGACATGGTGATA
 GTTGAACCTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACCAATCCCCTTGCTTATGTTT
 CAGTATTCGGTTCCTTGTCTGACTGATCAGTGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTGACTTTGCTTTGATTGTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAAAAACCTATTAACACAGTACCACAAGACTTGGAGAATTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCCTTGTCTCACTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTGTCTCATTGCGCCAAAGATGTCCACCTGGCTGCAATGTGAAAATGTGGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTACCCACGGCG
 GGCAGAATAGCATTAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAAGT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTATCTGCGCTCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA
 TGTCTTTACAGAGCCCTGGCATGAGCAGTACCTGTTGACGCTTTTTGTGTTTCTGCTGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACATAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTCTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTTCCAGTCTC
 CTGTGCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCCTGACCCTCAGATTTCCAGCCTTAAAAATCCACCTTCTCTCATGCGCCTCTCCGAA
 TCACACCTGACTCTTCCAGCTCCATGTCCAGACCTAGTCAAGCTCTCTCACTCTGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAGTTTCTGTTT
 TGTCTCCACATATTCTCTTCAATGTCTCAGGAAGCCTGCCCTGTGCTTGAAGTTTCAGGCG
 CGGACACAGGCTTCACAGGTCTCCACATTGGGTCCTGTCTGTGTCGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGATGAGAGCTGTAGGTTTCCAGATTCTCTGAAAAATAAAGTTTACA
 CGGTTATCTCTCCCAACCTCACTAA

10015386.121201

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
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```
><subunit 1 of 1, 523 aa, 1 stop
```

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFLEETLGGRGKFENLLNVLEYLALQCSHF LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSGFSLFGLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKLAELWFINSDFAFDFARPLLPNTVYVGGLEMKPIKFPVPQDLENFIAGFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHPLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPISIRLFVTHGGQNSIMEAIGHGVMPVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVLLRSHLSPLFTQRLGVWIDHVLQTGGATHLKPYPVQQPWHEQYLFDFVFFLLGLTGLTWLSCGILLGMVAVTQRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATTGTT
 CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCTGAAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCCTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACCGAGCCCTAGAGAGGGC
 AGACTATCAGGGTGCCGCGGCTGAGAATCCAGGGAGAGGAGCGGAACAGAAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTACAGGCCGCTCTGCTGGAGGGGAGTGCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGGCGGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTTGCTGCGGTCGGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTTGGCCTGTCTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGA
 CCTTGGGGACCGAGTGTCTCTGCGCTGCGTCGGGGGAATCTACTGGTGGTTGGAATACT
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGACCCAAAGTCTTTCAAGCACAGAAT
 CCAGCCCTGACAACTTCTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCGTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCACTTACC
 CTCCAGCCACCTGCTGCATCTGTTCTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACCTACTTTGCGGCCCTCTGCTCCTCCGTTTCCCCACCCAGCTTCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
 ATGGACAAGCCCTAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCAGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTTCTATGCTGGATCCAGATGGAATCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGAGGTATACAGAGCTGGAAGTGG
 ACCATGGAACATCGATAACCATGCATCCTCTTGTGTCACCTCCTGAACTGTCTCCAC
 CTTTGAAGTTTGAACCTTAGTCCCTCCACACTCTGACTGCTGCCCTCTTCTCTCCAGCTCTC
 TCACTGAGTTACTTCTACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCTCTGAT
 CTGTGCTGTCTTATTCTCTCTCTAGGCTTCCATTACCTGGGATTCCATGATTCTTCTCTT
 CAGACCCCTCTCTGCCAGTATGCTAAACCCTCCCTCTCTCTTCTTCTTACCCGCTGTCCCAT
 GGCCAGCCTGGATGAATCTATCAATAAAACACTAGAGAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGGAGAAGATCCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTCAGAGGAAAAATAATCAACTGTATACTAAAATTAAAAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECILVVCEFGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGEFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

10015336-21201

FIGURE 163

GCTGTTTCTCTCGCGCCACCACTGGCCGCGCGGCCGACGTCCAGGTGTCTAGCCGCCAGC
 CTCGACGCGCTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCGCGGGCAT
 GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCCGTGACTGGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCTACTCCGGGGTCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGACCTGCGCTGTCGCGCGAGGGGTCTGGGAGATGGGGCACT
 GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTGTGTCACCTGGCTCAATAGGTCCAA
 GGTGAAAAGCAGCTACAGGTCATCTCAGTGCTCCAGTGGGTCTGTCTCTTCTGTACTGG
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTTGGCTGGTGTTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA
 GTGGGTCCGAAACTGGGCTGTGTGGCGCTACTTTCGAGACTACTTTCCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACATATATCTTTGGATACCACCCCATGGTATCATG
 GGCTTGGGTGCCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCAGG
 CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGGACACCATAGACTATTGTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCTGCGGAACCGCAAGGGCTTTGTGAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTTCCTATCTACTCCTTTGGAGAGAATGAAGTGTAAGCAGGTGATCTTC
 GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCAGAAATACATTGGTTTCGCCCC
 ATGCATCTTCCATGGTCGAGGCCCTTCTCCTCCGACACCTGGGGGCTGGTGCCCTACTCCA
 AGCCCATCACCCTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG
 CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA
 CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCTGGAGGTGAAC**TGAG**CCAGCCTTCGGG
 GCCAATTCCTGGAGGAACAGCTGCAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGCA
 TGGGTGTCTGTGGGTTATTTAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 164

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIYVLYFTWLVFDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGGCCGGGGCGCGGGCGCCGCACTCGCTGAGGCCCGACGACGAGGCGGGCGGGCCCA
GGGCGGAGGAGCGCGCGGCCAGAGCGGGCCGCGGAGGCGACGCCGGGACGCCCGCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCTTGGGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCGCTGCTGGCCCTTCTGAAGACCCA
GTTCCGTGCTGCAGCTGCTGGTCGGCTTTGTCTCTGTGGTGAAGTGGTCTGGTCACTCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCGCTCACTGC CGCTCGCCTACTCACTCTGGAGCCA
ACTGCTCATGCTGCTGGAGTGTGGTCTGTCACGGAGTGTACACTGTTTACCGGACCGAGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGAGTCATCATCCTCAACCACTCTGAGATCGACTTCTCTGTGGTGGACCATGTGTGA
GCGCTTCGGAGTGTGGGAGCTCCAAGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTCTTGTGCAAGCGGAAGTGGGAGGAGCCGGGACACCGTGGTGAAGGCTGAG
GCGCTGTGCGACTACCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTACCGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGTGAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCGCAGTCAAGTGCCCTCGGGGGACAGTCGACGCTGTCTATGATGAACCTGAACCTCAGAGGAAA
CAAGAACCCTGCTCCCTGTGGGATCCTCTACGGGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCTCT
GGAAGACATCCCGCTGGATGAAGAGGAGCAGCTCAGTGGCTTCATAAAGTGTACAGGAGAGGACCGGCTCCA
GGAGATATATATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAAGCTGCCCGGAGGCGGTGGACCTCTCTGAA
CTTCTGTCTCTGGGCGACCATTTCTCTGTCTCCCTCTTTCAGTTTGTCTTGGGCGTCTTTCGACGCGGATCAC
TCTCTGATCTGACTTTCTTGGGGTTGTGGGAGCAGCTTCTTGGAGTTGCGAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGTGTGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCAGAAATTTCTGAGTTGAACCTGTGTAGTTACTGACATGAAAA
ATTCACTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGTTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAAATGAAGGAAATTAACAGCCTCAGAGACCCATGTTGACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAAGGAGAGGAGAGAAAGGTCAGAAAGATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACTAGATATTTTAT
AATCAAGTGTCAAATGACAAAGAAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTTG
ATCAGATTAAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCACTGTAATTTATTTGACTTTTGAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAAATTAGTCAAGCTTCTTGACCTGAGGAAGGCTGCTTTAGGCCGGGACAGCTGGC
TTACACCTGTAATCCAGCAGCTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACTCCT
GAGTTCAAGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGACGCGTGAGCCACTGCGCTGGCCGGA
ATTTCTTTTAAAGGCTGAATGATGGGGCCAGGCAGATGGCTCAGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCCACCTGCTGGCTAATTTTGTATTTTGTAGTAGAGCTGTAGCCAGGCTGGCTCTCGATCCTCT
GACCTCAAGTGACCACTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCTGAGCCACTGTGCTTGGCCTTGA
GCATCTTGTGATGTCTTATTTGCCATTTGTATATCTTCTATCTTCTTTGGGAAATGTCTGTTCAAGTCTTTG
CCTTTTAAATTTTATTTATTTATTTATTTATTTTATTTGAGACAGGCTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCTTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTGTATTTTGTATTTTGTAGCTGTAGTTTGTATTTTGTGAGGACAGCATTTCAACATGA
TGCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
CATGAGCCATGCACCTGGCAAACTCCAAAATTAACACACACACAAAAAACCCCTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCCAATACCAGGGAGACTGAAGTGGGAGGATCGCTTGGCATGAGAAGTCAAGGCTG
CAGTGAGTCAGAGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAGACCTGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVVSGLVINFVQLCTLALWPVSKQLYRRRLNCRLAYSLWSQLV
MLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCCATCACTCCCTCCAATGTCTTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCCTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
 GCTTACGCCTGATACGGCCCTGGGTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTGCTTCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCT
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTGTGTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTACCA
 GATGGTGTAGGGCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTGATTAGTAGGCCAGGTGGGCATCTCTAACAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACCTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTGTCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

101536.12101
 101536.12101

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCFSFALALGHFLISLVGKLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYITNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

10015336.121201

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAATACTGTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCAGCTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGCAAGCCCGAAGATTT
 CATAGCGGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGAACTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTATCACAAAGG
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTGGGCCAGGAGTCAAGGCCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGT
 TCAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
 TCCAAACCTAAGAACAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGTCAAGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAAATAAAAAAGAAATTATGGTTATTGTAA

1005336.121201

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

1015386.121201

CGGGGCCCGCAGTCCGAGACCTGTCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGCGCCATGACCAGCCGGTGCCCGGCTCTCCGTGCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCACTGGCCTCTTCTGGGGAGGCGG
GCCCCCATGGCAGGCCGCGCAGAGCAGTGCCTGCTTCCCCCAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGAGCTGGGACGGCCCTGTGGAGGCAGGCCAGGCGGAGCACAGATCGACCTCC
GGCTGAAGCCCGCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGCGACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAAGTGTCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGGCGAGCCGAGGCATCTCGCCGCTCTCAGATCTCTGTGGCGCGGAAGGTGCTGC
AACCTCGAAAGGGGACGTGGCGGCGAGTGTGTGCGAAACCTAAACAGCATCCGGCGG
GACGTGAGGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTTAAATTGAAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAFAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSR
MREHPALRSRLRLTLEQPGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRRLKPALETLELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

[illegible]

FIGURE 174

><subunit 1 of 1, 671 aa, 1 stop

MPHAFKPGDGLVFAKMGGYPHWPARIIDDIADGAVKPPPNKYPIFFGTHETAFLGPKDLFPYD
KCKDKYKGNPKRKGNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDRG
VMAVTAVTATAASDRMESDSDSDKSSDNGLKRKTALKMSVSKRARKASSDLDAQASVPSE
EENSESSSESEKTSQDQFTPEKKAARAPRRGFLGGRKKKKAPSASDSDSKADSDGAKPEFV
AMARSASSSSSSSSSSSDSDSVKPKPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGPPSSSDSEPAELEREAKSKAKPQSSSTEPARKPGQKEKRV
RPEEKQAKPVKVERTKRKSEGSFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALBEEQLTLQVTSQILQNLDTDVATLKKIRRYKANKDVMKAAEVYTRLSKSRVLGPKIEAV
QVKNKAGMEKEKAEELKGLLAGEEAPQKEADKPDSTDLSAPVNGEATSKGESAEDEKEHE
EGRDSEEGPRCGSSDELHDSVREGPDLDRPGSDROERERAGSDSALDEES

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ACACCATTTGAAACAGAACATTTGTTTTCATCAGTAAATGCTAATAAAGATGAAAGACTTAAAGCCAGAGCCAGA
 TTTTCACTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
 AAATATTCCAAGACTCAAGCTAACCTACAAGACTTCTGCTTTCAATAGCTGTATCCCTTTTGGGTTCATC
 AGAAGGACTGGATTTTCAACTCTTCTCTTAGATGAGGAAGAGGCAGGCTGCTTTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAACATTTATGGCCTGCTGCAAAAGAACGGGTGGA
 ATTTATGTAAATTAGCTGGGAAGATGCCAATACAGAATGTGCAATTTTCATCAGATGCTTCAGGCCATATACAA
 AACTCACATATATGTGTGGAGACTGGAGCATTTCATCCATATGTGGGTATATGTATCTGGAGTCTACACAGGA
 GGATATTATATTCAACTAGACACACATAATTTGAGTCTGGCAGACTGAATGTCTTTCGATCTCAGCAGCC
 TTTTGTCTCAGTAAATGACAGATGAGTACCTCTACTCTGGACAGCTTCTGATTTTCTTGGCAAGATAGTGCATT
 CACTCGATCCCTTGGGCTTACTCATGACCACCACTACATACAGAACTGACATTTAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTTGGAATTTTCTCATACAGACACCTTACAATCCAGATGATGATAAAATATATTTCTTCTTCG
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCACTCTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAAACGAGCCTGATAAACCAAGTGGACGACTTTTCTTAAGGCCAGCTGATTTGCTCAATTTCTGGAAG
 TGTATGCGGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAGAGATGAAAGAAATCCTGT
 AGTATATGCACTTTTACTACCAACCACTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAAATGGTCCATATGCTCATAGGAAAGTGCAGACCATCTGTTGGGTGCAGTATGATGGGAGAT
 TCTTTATCCAGGGCTGGTACTATGTCACAGCAAAACCTATGACCACCTGATTAAGTCCACCCGAGATTTTCCAGA
 TGTGTCTCAGTTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGATATACCAAGTTCGAGGAGGACCAACGTT
 CAGAGAATCAATGTGGTTACAGACTGCACAGATAGTGGTGGATCATGTCAATTCGAGAAGATGGCCAGTACGA
 TGTAAATGTTTCTTGGAAACAGACATTTGAACTGTCTCCTCAAAGTTTGCAGACATTTCAAAGGAAAGTGGAAATTTGGA
 AGAGGTAGTCTGGAGGATTCGAGATATTCAAGCATCTCATCATCTTGAACATGGAATTTGTCTCGAAGCA
 GCAACAAATTTGATATTGTTTCCCAGAGATGGATAGTTGAGCTCTCTTGCACAGATGCGACACTTATGGGAAGC
 TTGGCGAGACTGTTGCTTGGCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
 TTTCAAAGGAGAGCTAGACGCCAAGATGTAATAATGGCCAGCCCAATCACCAGTGGCTGGGACATCGAAGACAG
 CATTAGTCATGAACTGCTGATGAAAGGTGATTTTGGCATTGAAATTTAACTCAACCTTTCTGGAATGTATACC
 TAAATCCCAACAGCACTATTAATGGTATATCCAGAGGTGAGGAGTGAACATCGAGAGGATTTGAAGCCCA
 TGAAGAAATCATCAAAACGGAATATGGCTACTGATTCGAAGTTTGCAGAAGAGGATTTCTGGATGTATTTCTG
 CAAGCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCAATGAGAATGAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAGGATCTATTGGCTGAGTCAAGGTTGAGATCAAGAA
 CTACATCCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCAGTACTGCGAACAGATGTGGCAGAGGAGGAAGCG
 GAGACAGAGAAACAGGAGGGGCCCAAAGTGGAGCAGCATGCAGGAATGAAGAGAAACGAATTCAGAGACATCA
 CAGAGACCTGGATGAGTCCCTTAGAGCTGTAGCCACTGAGTTTCTACTAATTTAAAGAAAGAAATTTCTTACC
 TATAAAACATTTGCTTCTGTTTGTATATCCTTATAGTAATTCATAAATGCTTCCATGGATTTTGTCAAGG
 CACAAGACAATTAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGCCAAATAATTCATTGAAACAGTTT
 CCAAGACAATTTCTGAGCAAGCAAAAGTATAAGAAATATCCTAAAAATGAGGGGTTCACAGTTGAAATTTT
 TGTTTTGAATTTTGGAAATTTATGTCATGTAATAGTTGAGCTAAGCAAGGCTCGAAATTTGATAGTGATAGGT
 GCTTTATCCCTCGAATGTCATTAAGCATGGAATTTACCATCGATTTGGCTATGTTCTATGAACATATAT
 CATTCCTATTTAGAGAACAGCTACCTTGGTGGGAAATAGAGGCTCAGACACAAATTAAGACAATCCCATATC
 AACAGCAATTTCTCAGTGAGCCATCTCACTCTGGAGAAATGGTATAGGAATTTGGAAGGATTTGCAATTTCTTCT
 TGGCCACTGGGTTAAATTTAGTGTACTACAACATTTGATTTACTGAAGGCAATGATTTTCCAGGATTTTCT
 ATTGACTAGTCAGGATGAACAGTTTACAGAGAGAAGTTGGTCTTAGTATGTGTTTGTAGATATATACATAA
 GCTCTACGGCAGACAAATGCTTTATAAATACTTTAATAAGATATGGGAATATTTAATAAACAAGGAAACA
 TAATGATGTATAATGCATCTGTGGGAGGACATGCAGATGGGATTTGTAGAGACAGAGAGGAAGACGCCAT
 AAATTTGCTGCTTTGGGAAACATCATCTCCCATGAAAGGAGAGAACATCAAAATTAAGTGAAGTAAATGTA
 TGGAGCTCTTTTCACTAGGATATAGTAGTCCCAATTTGTAATTCATCTGTAAAAAAATCTAGATATTAA
 AACGCTCAGCAAAATCAGGAGAACTAAATCTTCTGAAGAAATCATAGGAGAGATGACATTTTATTTATAACC
 AATGTATTTTCAATGATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTTATTTTCTTCTG
 CTCTTTCTCTCTGATATTTGTTGATTTGATTTATTTGATGAATAGGAGAAACAATATATAACACACACGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGGATATATATTTGTTGAATTAACAGACAGTGTAAATTTTAA
 ACAGGAAAGGTTAAATTAACCTTTTGAATCTTCACTCAACCTTTCTCATGCTGAGTTAATCTGTTGTAAT
 GTAGTATTTGTTTGAATTTAAACAATAAATAGCCTGCTACATGT

10015386.121201

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
 ><subunit 1 of 1, 777 aa, 1 stop
 ><MW: 89651, pI: 7.97, NX(S/T): 3
 MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
 GSSEGLDFQTLRLLEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAKERVLCCKLAGKDA
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNKAKFIGTFF
 IPDTYNPDDDKIYFFRESSQEGSTSDKTILSRVGRVCKNDVGGQSRSLINKWTFLKARLIC
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSACVYSMADIRAVFNGP
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFDDVISFIKRHSVMYKSVYPV
 AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISEKKNMEEVVLEE
 LQIFKHSSIILNMLSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCLARDFYCAWDGNA
 CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTN
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQLSSPNFSLDQYCEQMWHREKRQRN
 KGGPKWKHMQEMKKRNRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

1001536-121201

CTACACTCCCTGAGCCCACTAGCTGGAAGCCGCGAGGTCATCCTGGAGCATGCCACGCGGGGAGCAGCA
GACCTCCAGAGTAAGCTGGGACAGCAAGCTAGACTGTTCTTCAGGAGCCTGGTGATTTTCCCCACCCCAAC
CTCAGACAGTTTCAGCCAGCAGGAGCACTCAGTCAGTGTGTGCTCGTAGGCGGGGAGAGGCGGTGGCTGGCAAG
GTGGGCTCGGAGAAAGAGGTTTCAGCGCTTGACCACCGAGAGCTGCCCGTGACTACAAGATCCAGACCAATGGGCATCT
GGTGAGTGCGGGGGGACAGSTGTTCATGTGCACTTCTGTCTCAGCAAGAAGAGCTGAGAGCAGGGGATCTGG
AGCCATTGAGGGTGTGATGGAGCTACAGAGGGGGAGGAAGGTTATTTAAGTAAACAGTGTGCCACATAGGTAA
GAGACAGATTTTGGAGTGATAGCCAGCAATAGGTTCAAACTTCTCTGTGCTCTAGTTTGTGTAGCCCAAGT
AAGGAGAGTCACTTAACCTCTCGCATCTCAATTTCTCATCATCAAAAGTAGGGCCCAATAGATGACCAACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGTCAGCACTAGCAAAATACAGCTCCATATAGTCATGTGCCCAAG
TATTTTCCACCCACCCCTGTTCTCTGCTGCTCCCAACAGAGTACTGCACACAGCTTGAGGACAGAGCGCGGACAGGCT
CAGAGCGGGAGGCTTCAAACGATACAGAGAGGTTACAGAAAGTCGAGAGAGACATCCGCGAGGACAGTGAAGC
AGGTGAAGGGGGCTGCCCGGCTGGCCGCTCTCGAGGGGGCTGGCTTGATGTGGAGGCGTGGCTGAGCCAGCA
TGACCCAGGCCAGGATAGGTGAGGACGAGGAGCGGCGCTCAGTAGGGCTGGCTGTCCAGAGAGGCACTTCTC
CAACCGCTAGGAGTGTGATGGTTCTTCACTTGACCTTGAAGGATGTGAGGAGACGGGAGAGCTCTTGAGGAGCCTGCC
CCAGGCGCTGGCCACGAGGCTCTCCCTGCCCTGCACACTGGTATTTCGCTATCAGGACGGCGTAGGATGT
AGCTGACAACTCAGGAGGCTGATGTGCTGAGGTGATACAGGAGGGAGATGCTGACAGAAATGGTGCAAGGCTCGA
ACACACACGGGAGGATAGCTTTGTCCTGAGCATATCTCAACTTCCCGGAGACTCTCTCCTCCAGAGAGCAGCG
AGACAGTGCACAATCCTCGCGGGCAGAGGCCACAGCAATCTGGACAGAGGCCCTGTACAGTACACACGGGACAG
TGCAGAGGACCTGAGCTTCCCTGAGGGGCGCATCATCCGTCTGCTGCCCGGGGCCAGAGTGGATAGTATGACG
GCTTCTGAGGGGAGAAATTGGGGGCGATGTGGGGTCTCCCTCTGCTGGTGGAAGAGCTGTGTGGCCGCC
CAGGGCCACCTGAATCTCTGACCTTGCACAGATGTGCGGCTCCCTCTCTCTCCAGGCTTCTCCCACTCTGCAC
CTACCTCTGTGTGGATGGGCCCTCTGCATCTGTCTGCTGGGACAAAGCCCTGCAATCTCCCTGGGTCTGGC
ACATGATGGCACTCGACTCAGGCGGCTGCTCTCAACAGCTCCCGCCGGCTTAAAGCCCGGATCTGTGCCAC
CGAGTGTCCCTACCTGAGGCGCGAGGAGCCTTGACCCCAGTAGTGTGCTGGCTTATCTCAAGCTGTGAGA
CAACACCAATCAATGATTCAGAGCAGACAGCCAGCAAGCTGGAATCGCCCTTATTTCAACCTCAACCTCAAGGCT
GAAACTGTGCCCTCCCATTTCTAGAGCTGGAAGCCCACTCTTTTTCATTTCTTATCACTTCATGAGGAC
GGAACACTACCTTCTCTTGTGTGATCAACCTTACTAGGGTGGTGAAATGGCTGAATCTCTGGGGCTGGAAGC
ATCCATCAAGGTCTCTAGTAGTGTGGCCACCTCTTCCCACCTGGCTTCAAGTACCACCACCTCTGAAATG
CAGGGTCACTGGGGTGTGGGCTGGGAGAGGACAGCCGCTTGGGAATCAGGAGCTGAGGACCGAGTGCAGAACAG
CTGTAAATGGTCTGACGGGATTTTATGCAATGAATTAAGGAGCAGGAAGGCCAGGCCAGGCGCTGGGCTCTTGTG
CTAGAGGAGCGAGGGGCTACGGTGTCTATGCTTTAGGGGCGACACAGCCGCGAGGCGCTCTGCCAGCTGCCAC
GCTATCTCATATGAGCGAGGATGTGGGAGAGCGGGGAGGCGGCTGTGACGACGCTGGTGGGAGGAGCAAGAGAC
TAGGGGCTGTGACCTCTCTGAGGCGCCAGGCTGAGACTGTGCACTCAGGCTGGAAGTAGACCTGTGCTCT
AGCTGGGGGCGATGCTGTCCAGTGGGAGGAGGAGGCTTCAACGCCACCCACCTGCCCTGGCCCTGGCAGTGTGAG
TCCATCAGCACAATGAAGAGACTGTGAGAAGAGGAGAAATAACACTGTGCTCTGTTCAAGCTGTGTGCAAG
TTTTCCTGGGGCTCCAGGACTTCTCCTACTCTCACCACCAACCAAGGATTATAGCAAGGCTAGGCTGT
AGTTTACTCTGGGGTTCAGGAGGCCGAAAGGCTTAAATAGTTTAGTAGGTGATGGGAATGAGATTACCTCA
TTTAGGCTCAGGCACTACCTTCACTATCTCCCTCGCTTCTGGTAGAGACACTCAGAGAAAGAGGAGGGG
TCACCAATCAGACAGCAGGAGTAGCTCATCTCAGTGGCCGCCAGAGTAGAGAGCAATTAAGAGCCAGCGGAGGCT
ATCTCCCGCTGTGTTTCTCACTCTGTGATCAGAAGTGTGCTGTGCTGGCTGGCCATTTGCTCTTGTAGTGT
CGAGCCTCTGGGCTTGGGCTCCTCCTCGGCGCTCAGTGTGGGCTCAGAGAGCTCTGGGGTTCCTCTCAAGT
CAGAGAGGGTTAGGCTGTCTGCTGAGTCTCCATTTGTACTGGGGGGCTGGCTAGGACCTGGGCTGTGGCC
TCTCAGGGGACGCTCTCATGTGCGAGGATCCCTGCTTGGGCTCGGCTCCCCAGACCTTGACCACCCCTCG
GGTCTGTGCTCCCCACAGAGCCAGCTCTGCTGTGTGTGGGGGAGCTACAGGTTGTCTGTGCAATGAGGCT
TCTCAATGTGTGTACCCGCAACTGGGAGGGGAGGAAACACTGGGTTTAGGACCACTCAGAGCTGTGGT
GCCCTCCCTCTCAGCCAGGACATCTGAGTTTGGTGGCTACTTCCCTGGGCTAAGGTAGGGGAGGCTCTC
AGATTGTGGGACATTTGTGTAGGCTGACTCTGCTGGAGTCCAGTCCAGAGGAAAGAGCCAGGCCCACT
TTGGGATCAGGTGCTGATCACTGGGCGCCCTACTCAGCCGCCCTTTCCCTGGAGCGCTGCCCACTGCCCA
CAGAGAACAACAGTGTCTCCCTGTCCGGGGGCGGCTTTTCTCTCTTGGAGCGCTCCTGACGCAAGGTGAG
GCTCTTGTGCTGGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTATGATGGGAGGGGCT
GGCTCTCGAGGCTGAGGTGGCATCCACACTGACAGCAGGAGGGGAGTGAAGGTACATTTTTCATTTCTCT
CATGTTTGTGTTTCTACGTTCTTTCAGATGCTCCTTAAACCCGAGCCCAATTTCCCCAGGCCCAATTT
TTCTTCTGCTTTCTCAATAAATCAATATTAAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFQAGREDELTITEGEWLEWIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPPAFTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

101536-12101

ACAGGGAGACCCACCAAGCTATTATGCACGAGAGAGACAGAGGAGCGAAAGAGACAGAGACAAGGCCACAGCGGAA
GAGGCAGACAGACAGGCGAGCAGACGAAAGCCGGCCACAGAGCTCTACAGAGGGGAGAGGCCACAGAGAGCTGCAGA
AGACACAGGCGAGGAGGAGCAAAAGATCGGGAAGAGAGGCTCTAGGAGAGAGATTTGGAGAGACAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACATAGTTTCTCATTTCTCTTAAGCGTCTCAGCCCTCTGTAAATATTTGGC
TCTGACCTTGGCAGGAGTCGAAGCCGCCAGCTCAGACGAGAGCTTTCCAAAGTAGGGTGTGGAGGACTTTGGC
GCCCTAGAGCGGCTGACCTCCCTCCAGCTCAGTACCACTGCCATGTCAGACAGAGCTGCATCCCGGAGAGGG
CTTGGAGGCGGCTGGCTGTGGGAGGCCAACAGCTGGCTCTGCTCCCAATGTGGCGCTTCTGGTGCTGTGTGT
CTGCTCTTGCTAGTACTGTGGCTCTCTCTGCCCTCAGCCGGCTGGGCGAGCCCTCCCGGAGGAGGAGAGAT
CGTGTTCAGAGAGCTCACAAGCAGGCTCTGCTGCTGCTGGGCGCCCTTGCAGGCTGTGTGGCGCTGTGC
GGCCTTTGGGAGAGCTGCTACTAGAGCTGGAGCAGACTCCGGTGTGCAGGTGAGGCGCTGCACCTGCAGT
CTGGGCGAGCGCTGAGCTGTGGGTGAAGCAGAGCTGCGCACTTCACTGACTGGCCACCATTAAGGAGATCC
GGAGTCGGTGGCATCTTGCAGTGGGATGGGGAGGCCCTGTTAGGCTGTTACAATATCGGGGGGCTGAATCCCA
CTCCAGCCGCTGAGGGAGGCAACCCTAACTCTGCTGGGAGCTGGGCTCACATCTCTACGCGGAAGATGCC
TGCAGCGGTCAAGGTCCATCTGCAAGCTCAAGGCTCTCTTGGAAAGCCCCAGCCGACCCGAGAGGCCAA
CGCTCTTGCTCACTAGTAGATTTGTGGAGACACTGTGTGGCAGATCAAGAGTGGCCGCAATTCGAGCTGC
GGGCTTAAAGCCTACCTGCTAACAGTGTGGCAGAGGAGAGGCTCTGACAGAGCTCAAGAGCTCGCAATTC
TGTCACTTGGTGGTGACTCGGCTAGTAGTCTGTGGGTCAGGAGGAGGGGCCCAAGTGGGGCCAGTCTGCG
CCAGACCTTGGCAGCTCTTGTGCTGCGAGCGGGGCTCAACCAAGCTGAGGACTGGGCGCTGACCACTTTGA
CACAGCACTTGTGTTACCGCTCAGGACCTGTGTGGAGTTCTTCAATTTGGCAGACGCTGGGTATGCTGTGGG
CACGCTCTGTAGCCCGCTCGAGCTGTGCATTTGTGGAGATGATGGGCTCCAGTAGCCTTCACTGCTGTCA
TGAATCGGCTCATGTCTTCAACATGCTCCATGACACTCAAGCCATGATCAGTTTGAATGGGCTTTGAGAC
CTCTCGGCTGTATGCTGCCCTGTGATGGTGTATGGATCTGAGGAGCCCTGGTGCCCTGAGTGGCCGTGT
CATCATGACTTCTTGCAGCAATGGTATGGGCACTCTCTTAGACAACAGAGGCTCAATTGCATCTGCTGT
GACTTTCTCGAGAGACTATGTAGTCTGAGCGCACTGCTGAGCTGACTCTGGGCGCGACTGACGCCATTTGCC
ACAGTGTGCGCGCGGCTGTGCTGCCCTCTGTGCTCTGCGCACTGATGAATGGCATGCCATTGCCACAGAACCA
CTCGCCCTGGGCGGAGTGGCAACCTCGGCCGCCGACAGGCTCGAATGGTGTGCTGCTCTGCACGGACCA
GCTCCAGGACTTCAATTTCCACAGGCTGTGGCTGGGGCTTGGGCAAGTGGGCTGACTCTCTCGAGCCTG
TGGGGTGGTGTTCAGTTTCTCTCCGAGCTGAGTGCAGAGGCTCTTCCCCGGAATGTGGCAAGTCTGAGG
CCGCGCTAACCGGTTCCGCTCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGGGAGGAG
GTGTGCTGCTCAACCAACCGCAACGCTTCTCAAGACTTCCAGGCTTCCAGGCGCCATGGAATGGGTCTGCTGCACAC
AGGCTGTGCCCGCCAGGACCACTGCAAACTCACTTGCAGCGCCGGGCACTGGGTACTACTATGTCTGGAGCG
ACGGTGTAGTAGGAGCCCTGTGTCGCCGACGCTCTCGGCTCTGTGTCAGAGGCGGATGCATCTCTGCTGTG
CTGTGATGCATCACTTGGCTCCAAGAAGAGTTTACAGATGCAAGTGTGTGGAGGAGGAGCGTTTGGTTGACAG
CAAGCACTCAGCTCTCTCAGGAATTCAGGTACGGTACAACAATTTGGTCACTATCCCCGGGGGCGACCCA
CAITTTCTTCCGCGCAGCAGGAAACCTTGCCACCGGAGCACTACTTGGGCTTGAAGCTGCCAGTGGCTCTGA
TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGCACTCAGTTCGCGTA
CAGCGGGGCGACTCGAGCTCAGAGACACTGTGACGAGTGGGCACTGGCCAGCTTTGACACTCAAGTCTT
AGTGGCTGGCAACCCCGGACAGCAGCTCCGATACAGCTTTCTGTGCGCCGGCGCAGCCCTCTCAACGCGAC
CCCCATCCCCAGGACTGGCTGCACGGAAGACAGAGTTCTGGAGATCTTTCGGCGGCGCCCTGGCGGGGAC
GAAATAACTCACTCATCCGCGTCCCTTTCTTGGGCAACGGGCGCTCCGACTTGTGGGAGAAAGAGAGACTT
CTGTTGGCTGCTCATGTAAGACTCAGTGGGAGGGGCTGTGGGCTGAGACTGCCCCCTCTCTTGCCTCACT
CGCAGGCTGGCCCTGCCCTGTTTCTTGCCCTGGGAGGAGTGTGGGTAGTGTGAATGGAGGGGCTGACAGC
AGCCCTCATCTAAACTGCCCTCTGCCCTCGGGTCAAGAGGGGAGGGGAGGACGAGGAGGCGCTGGGCC
CAGTGTGATTTTATTGATTTTATTCACTTTATTAGCAAGGGAAGGGGACAGGACTAGGCTCTGGGAA
CTGACCCTGACCCTCATAGCCCTCAOCTTGGGCTAGGAATCAGGCTGGTGATGATAGTAAATGAGTGGT
TGTGATCGGTGGTGTGTGTGTGTAATATGTGTCTGCTATGATAGTAGTACAACCTGTCTGCTTCTCT
TTCTGAAATTTTATTTTGGGAAAGAAAGTCAAGGTAGGCTGGGCTTCAGGAGTAGGGGATATCTTTT
TTTTTTTTTTCTTTCTTTCTTTTTTTTTTTTGGACAGAAATCTCGCTCTGTGCGCAGGCTGGAGTGAAT
GCAAACTTCGGCTCACTGACTCTCCGCGTCCCGGTTCAAGTAGTTCTCATGCTCAGGCTCAGGCTCTGATGAGTGT
GAAATACAGGCTCTGCCACAGCCCGCAATTTTGTGTTTGTGTTAGTGGACAGAGTCTCGCATTTGTC
ACAGGCGTGAATGATTTCAGCTCACTGCAACCTTCGCACTGGGTTCAAGCAATCTCTCGCTCAGGCTCT
CSAGTAGCTGAGATATAGGCACTTACACAGCGCCGGCTAATTTTGTATTTTATGATAGGACGGGTTTAC
CATGTTGGCCAGCGGTGCTCGAATCTCGACTCTTAGGTATTCATCTCGGCTCAGCTCTCCCAAGTGTGGGAT
ACAGGCTGAGGCAGCTGGCTGGCAACGCCAATAATTTTGTATTTTATGATAGACAGGTTTCAACATGT
TGGCAGGCTGCTCTGAACTCTGCAGCTCAGGTATGACCTGCTCGGCTCCCAAGTGTGGGATACAGG
TGTGAGCACAGCGCCGCTACATATTTTAAATTAATTTACTAATTTATGTATGATCTTGTGGATCAGACAG

FIGURE 179B

ATGIGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

1015386.121201

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGRLAGRWLGAQPCLLLPFIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNQSVLPQSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPPELLGGAEP
GTYLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGGQPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPQVGPAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLQGVSTCDTLGMADVGTVCDFARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSTRHCPQLFPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRRTFRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPODQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVLVPLGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPDWLHRRQAILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

10015386.121201

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGGTTGGTATCCTGGCCCTAACTCT
 AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATCCAAAATCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGCATCATGCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCTAATAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

1001336.21201
 1001336.21201

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEIEFDPLMDERGYCCICYCRGNRYCRRVCEPLLGYPPYPICYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACCCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTTGCTTTGCCTGTCTGCCAGGACGAGGCACCTTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGT
 TGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

1015336.121201

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTTILPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLLCLSCQ
DEAPYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

1005386-12401

FIGURE 185

GAGCTCCCTCAGGAGCGCTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTGCCAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTAGACACAGGTACACATTTGGTGGCGTCTGTTCTGTG
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCTGCCGGGG
 CCTGGCACCAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAA
 AACAAGGAGATCCCCTAGATTTCTTCTGCTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTTCTCTCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCAAGAAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGCTCTCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAAGTTACCAACCAAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATATTTTTTTTAAAT
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCGAGAAGTTCGAGACTAGCCGTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCACGGG
 AGGTTGGGGTGCAGTGAGCCATGATCACACCACTGCACCTCAGGCAGGTGACATAGCCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTTAGGAAGTGGTTAA
 ACTAATTCTTTAA

1005336.121201

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

1001336.12101

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG
 GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAAACAACATCGTGGTTTTTGAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGTCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGGCCATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTAACTTTACTATAAAGC
 CATGCAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTATA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCGAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAATAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTCTGATATGCTG
 TTTTTTAGCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCCTGTGTATTAAATTAACATTTTAAACGCAGATATTTGTCAAGGGGCTTTCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATAATAAATAAAGAGCAGAAAAATATGCTTGGTTTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCTGTGAAAAATAAATTCCTTCTGTACCATTTCTGTTAGTTTTACTATAA
 ATCTGTAATACTGATTTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGTGCTTTATACATTTATA
 TTAATAAATTTGTACATTTTCTAAT

1005336 "121201

FIGURE 188

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGGCTTGTCTGGTCTACCTTGTGTTGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCACTCTGGGA
TTGTCTTTGTCTCTCAGGGGTCCTGACGCTAATCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGTTGTCTGTCTGCACTT
GCCCCCTCGGGGGGTCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT
GCCATCTCTCGGGGGCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTGTGACTGAGGATATTTAAATTCATTT
GAAAACCTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCGCCCAAGAGTTCTTGCTGCTGCTGGGGCTGGGCTTCCCTAGATGTCACCTGGACAGCTG
CCCCCATCTTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCTCCGTCCTGATAAGACG
TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTTTACACTCACATTTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

1015386.121201

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIRDFYNPLVAEAQKRELGLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAIRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

101536-12101

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTATATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTCGAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAACAGCCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
 ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACITTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
 GAAGCAAGGTACAGATATCCAGTGCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
 GAACCTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATCAAGTATACCCATAATCATTAGCAAG
 GTGACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

101536 121201
 101536 121201

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

10015386.121201

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCAC TTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTTCAGTTTCTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTGAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

10015386.121201

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

10015386.121201

CCCGCGCCCGGTTCTCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCC
CGCGGCCATGGCTGCTCCCCGCGCGGCTGCTGTCTTGGCCCTGACCGGGCTGGCGCTGC
TCTTCTCCTGTGCTGGGGCCAGGTGGCATAAGTGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAACATAAGACTAAAGTGGCGGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCACGGCTTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCTCAATAGCCTTACACTACTTGGTTTCTGATTTCGCTCTATTTCAGCAGAT
CTTTTCACCTACTTTGTGTGATCAAAAAGAGAGATTAACCAACACATGCTAATGCCTTT
TGATATTTCATGGGAATGCCCTCTCACTTTAAAAATAAGAAATAAAGCATTTTGTTTAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

10015336.121201

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCTCTTTTCTCGGTGCTTGCTGCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCAGGCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
CCCCGGACTCCCCGCAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTCACCTCCCTCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGTTCCC
CCAAATCCCCCTTGCCCGCCGGGGTCCGAGCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCTGCTGCTCCTGCTGTGTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCC**GTAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGGGCGGAGCTGCTGCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGCTCGGGGCCACCTCCCGGGCTGCTGAACCTCAGCCGCA
CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCTGCTCGCCCCCGGGCAGAGCCG
GGCCGCCCCGGGGCCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCCTCCAATCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGCGTGCGGAGGTGGTGAAGGGGAGCGGGAG
GGGCAGAGGAGTCCCCGGAACCCGTGCAGATTAAAGTAAGTGTGAAGTTTAAAAAAAAA
AAAAAAA

1005386.121201

FIGURE 198

MTLIEGVGDEVTVLFSVLACLVLVLAALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPADPSQPEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFFGREQQVRLIYQGQLLGDDTQTGLSLHLPNCVLHCHVSTRVGGPPNPCCPGS
EPGPGSGLEIGSLLPLLLLLLLLLLWYCOIQYRPFPLTATGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCTCCCCCTCAAGGATGACAAAGGCGCTACTCATCTATTTTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTTGGCCAGGTGCTGCAGCT
GGAGGACTTTGGATGGGTTTGAGGGTTACTCCTGAGTGACTGCTGTGCCTTGGCTTTTGTGG
AAAGCAAGTTCAACATATCAAAGATAAATGAAAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCAGATCAACAGCCACTACTGGTGAACAGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTACAGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCCGTGAGATGAAACAGGGTGCGGGTGACCCGTGG
AGTCATTTCCAAGACTCCTGTCTCTACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA
CTTCATTGTATTATTTCTTCTCTTCCATTTAACAATAAACTGACCAGAGCCCCAGGAATAAA
TTGGTTTCTTGGTCTTCTCCTTACTCCCATCTGACACCAGTCCCGCTGCTGTGTATCG
TTGTAAACTGAGGACCACAATAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

10015386.121201

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGGAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATT
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCCGTGTGGTTTTCTGATTGTAAGTGGAAAGCAGGCTTTGCACACGCT
 TGTGGCAAATGTGAGGACAGGTTAAGTGACTGGCAGAAAACCTCCAGGTGGAACAGCA
 ACCCATGTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAAGCTAACTTGAACATGAC
 CTGTTGCACTTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTGCTGCTCTCTGATGCTGGGATGCCGTCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACACACCTTGCACCGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCCTTACCCAGGCCAGAAGGAACAGAGCCAGGCAGGAGAGGTGGG
 AGCTACGCCCTCATCAAGCAGCAAGGAGGCAGGATAAGGAAGCCCCAAAGGGGACTGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGAGCCTGGACCCAC
 GTGGCCTCCAGAGGCCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
 CACCCACTGTGTCTGACGACACCTCAGGACAGCCTGCCACAGCCAGCGTCACTCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCTGACACAGTGC
 CCAGGCGCTTCTGGAAGGAGATCATCTCTGTTGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTTGGACTGGAAGCTGGATTTCCACTGGGAAC
 CTTTGGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAAGTGTCTTTCAAGGCCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTTCCAT
 TCCCCCTCGACAGGAGGCCACCTCGAGGAACAGGGTTCGATCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCTCTCTGTCAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAGGAGAGTGGGTGTGCGACATTTCCACTGG
 TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGCTCACCAGCAGCATGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTCAAGAAAAAC
 AATAAAGATTGTACTGCTCCGTGTGATGGAAAAGCCCGCCAGCAGTGCGCATTTGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCAAAGTGAACGTAAGAGCTTATATATTTCAATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTGTGTGTAGGAGAGAAAAAGCTCTATGAAAGAAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

10015386.121201

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRWDGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVVSF
VIDVIDWKTFFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGGSVEILPCSRVGHYIQNDSSHSPLDQEATL
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRIGCRTFWHFLANVYPEL
YPSEPRPSFSGKLNHTGLGLCADCQAEGLGCPMVLAPCSDSRQQQYQLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIHVHILSGKCMEEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGTGTAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGTGTCTGTCTCCACCTCCTCCCTCTCTGGCCACTGCTGTGTC
 TGCCCTCCACCCGCTGTCTCAGGGCTCTTCATCCTCCCCTCGAACCCACCAGCCCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTATGTGTGCTGTGGAGCGAGC
 ACCTCCACCAAGCGCATCTCCTCGGGTCCCAAGATCACGTGCGCAAGTCTGCTTGGCCACTG
 CACCCCGACGCCACCCATCAGGCTTTGAGGAGGGCGCCCTCATCCCAATACCCCTGGGGCT
 ATCGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTTGAGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCTGCGGCCATTC
 CTGTTTCGGGGCGTGGGGAAGGTGTGGACCCCGAGTCTATGTCACAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCTCAGGCAGCAAGGTGCCCTGAGGCAGGAGGAGCCAGCAGCCACTGACA
 GACCTGTCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACCTACCCCAACCC
 TGACCATGAGGACCCCGAGGGGACCCCGCCTGGGATGCCCAACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAAGGGCAGGGGCAATGGGATGGGAGGCAAGAGGGAAGGCAAC
 TTAGTCTTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTATGAGGAGGCAGGCGTGGC
 CTCACAGCCCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATCTCTGCTGCCATAACTCCAACCTCTGCCC
 TCTTTGGTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCACT
 TCCCTCTTCTCTCAGGATTCCCTTGGTGAATCTGTGATGCCCAATGTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCCATCCACTGAGGTTGGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCCCGGAACACTCCCCAGCC
 CCACGGGCAATCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACAATCTGTGACTTCG
 GGTCCCTGTCCCCACCTTGTGCACCTCACATGAAAGCCTTGACACTCACCTCCACCTTAC
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTGCTCACATTTGCACTCTCTCCTTCCACATTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTTCTGCACACTTTACCTCTCATGTGCGTTTTCCCGCCCTGATGTTGTGGTGG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTTCCGACGCCCTGC
 GTGCTGCTCCAGAGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCACACCAATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTACCCCCAGCCCA
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTGCCTGCTGCACCTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGCTTTGCTGTCTCCGCTG
 TCTGTGTGTGTGCCATTTCTGGACTTCAGAGCCCCCTGAGCCAGTCCCTCCCTCCAGCCT
 CCCTTTGGGCCCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCAGCTGGTTCAGGGC
 ATCGGGAGCTCTGCTCCAACTTACCCCTTCCCTTCCCGGACTCCCTCCTGTCCCCCTCTTT
 CTCCTCCTTCTCCTTCACTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT
 CTTCCTCCTTCTCACATGGTTTTTCCACCTTCTCTCTTCCCTTCTTCCCTTCCCTTCCCTTCCCT
 GTGATATATATTTTTGTATTATCTTTCTTCTTCTGTGGTGATCATCTGAATTACTGTG
 GGATGTAAGTTTTCAAAAATTTTCAATAAAGCCTTTGCAAGATAA

10015386-121201

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAA SPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCS DYPKG DASTGWNSVSRIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCCTGGCCCTGCGGTG
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGGCCCCGTGGAGAGCACCAAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
 GGC GGCTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGGTGTCTGGCGCTCGTGGTCTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA
 GGGGCCGCGCCCGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA

10015336.121201
 10015336.121201

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGCTGTGCCTGACGGCGGCGCTGCCCCA
 CGGCTGTCTGCACCTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCGCGGGGACCTCCCCTAAGTAGCCC
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTCCCTCCGGGCCATGGACACACATACATGAAACCAGGCCGCAT
 CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG
 ACTCGCACGTCGCCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCGCCTTCCAC
 CTGGCTGTATCGGGTAGGGCGGGGCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT
 CCCACAGGTCTCGGGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
 TGGCACAAGTAAGTCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGCTCTAGAGGGGCTCCGGA
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCTCAAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCCATCCCAGGTCTGTGCTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTGAGACAGGACACGAGCATGAGGTAAGGCCGC
 CCTGACCTGGAATTGAGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGAACACACCCATGTGTTGGTTTCATGAACAGACCAGCTCCTCTGCCCTTCTCCTGG
 CCTGGGACACACAGAGCCACCCCGGCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCCTGCACACCCTTCGGACATCCCAGGC
 ACGAGGGTGTGTTGGATGTGGCCACACATAGGACCACACGTCCTCAGCTGGGAGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATGCCAGCCCTTAAGGTGTCTGGAGCCCCACACTTGCCCAACCTGACCT
 TGGAAGATGCTGTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCCTGCCAGGGCAAC
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTGTGAGCTGGGCTGGCTGCTGCTG
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
 GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCCGACAGACTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

1001536121201

FIGURE 209

AGCAGGAGCAGGAGAGGGACAA**ATGGA**AGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTC
 CCTCACGTGTGAGCTGGCTGCAGAAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCATACTCCA
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTTAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCATCTCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGAATTTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAATTTTGTGATGGATTCTTAAGTGGAAAATTTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACTCT**TGA**CTTCTCCTTGGAACATACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCACACACACACGACGTCACACACGCAACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTCAATATCTCTCACTCCCTATCCAATTTCTTCTTATCGTGCAAT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTTGCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCC
 TATGTAAATCAACAACCTGCATAATAATAAAAAGGCAATCATGTTATA

1005336 "121201

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEEVEKSSDGPAAQEPTWLTDPAAEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQKGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

10015386.121201

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGAGCGCGGCGTGGAGGTGCCACCCGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCTGTAGAAAAGAGAATTTGCCTGTGTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 CTGTGGTCTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCAGTCATATATGCACAGTTAGACCCTCCGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTTCTTTT
 AGGTCATTTACAATTGGGAGATTTAGAAAACATTCTTTTACCATCATTTAGAAATGGTTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTCTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
 AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAAGGATAATGCCGAAG
 GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTA

1005336 "121201

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGTCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

10221335612401

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTGCAGCAGTGA CTGCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCGCGACCCCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAGAGAAATGTTGCATTTGAGCAAGAAAAAGAGGCAAAAGTAATGAAAAGAAATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTGAGAGAAAAGTTTGAAGATTCGAATGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTTGGA
 CTATATGCAAGAAAATATCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTACAAATAGAGCAAGGTTAAATGAATACCTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAAGTAAAAAA

1005386 "121201
 1005386 "121201

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

10015336-12401

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTTCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCTGGAGATGGAACAGGCCCAAGAAGGCCAAGAACCCCAAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATCACTGCTCACTTGATACGTTATTCAGAAACCCAAG
 GAATGGCTGTCCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

101536 21801
 101536 21801

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSFVPACSLVESHLS DQLTLHVDVAGNVVGVS VVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQE QKSFFAKYWMIIPVVLFLMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

10121"986001

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGCCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCAGGGGCGAGCAGGTGCTCCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTTGGATTGGCTGGGTC
 GCAAGAATTCTTGCTCCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTGGCCCTTCGAAACTGGGGGGAGAATATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGCGGACCGCCGC
 GTGCTGTGCTGGGCACCATAACAAGCTCTATTGAGAGTGTATCTTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACGATTTGTCTGTG
 CTGTCATGGTGATGGCTCTGTGTCAGTGGTGGGACTCTTACCGTGGAAGGCATGATGCT
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCCGTGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

10015386.121201

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLLIELACGLYFPSMSFLRRKVI PET
 EQAGVLNWFVRVPLHSLACLGLLVLHDSRKTGTRNMFSCSAVMVMALLAVVGLFTTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGCGGCGGAGAGGAAACGCGGCGCCGGGCCGGGCCCTGGAG**ATG**
 GTCCCGGCGCCGCGGGCTGGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCTCCGCTGAACCTCCAGAGGCCTGCGGGGAAGTACAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
 CCATCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTACTGACTTTTGTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

101336.121201

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISSIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

100536.2101

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACCTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAAATGGCTGTGTTTAAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

10015336-121201

FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
 GGTGCCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
 CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
 GGCCCTGGAGGAGGCAAGTATTTAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCT
 GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
 ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
 ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
 GGACCGCTATTTCTATTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
 AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
 TTGGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
 AGCAAACCTACCCGTGGGTGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
 GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAAGTCGGGACGCTGAATCTGAATCCACCAATA
 AATAAAGCTTCTGCAGAAAA

1005386.121201

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKISIGFEWNYPLEEPTTEPPVNLTYANSFPVGR

Signal peptide:

amino acids 1-22

10015386 121201

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTTAGGATCCAGTT
 TTTTTTTAAACGCCCTCCACCCCCCAAAAACTGTAAAGATGCAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCAAAGGGGTCCAATTTTTCTTCTGGGTGTGACGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTATGCAACTGGCCCTTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGCGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCAAGACTGCCCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGTTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCTAG
 GACAGACCATGTCTGACCTGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACATGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCAGGCGCAAGCAT
 GAGAGCAAACCCCTTTGCCCGGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACCGGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTGATGGAAGCGGTACCTCGGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCCAGCACCCAGGAATTTATGTAGATTATAAACCCACCAACACGAGACCGAGCGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTCTTTATTGAACCTC
 TGGTGACTATCAAGGGAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTGTCCGTTTTAGTGCAATTCATAACTGGTCAATTTTCCCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAATCAATGTGAAGCTTGAACCTCCGTTTAAATATAA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAATGTGCAATTTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAA

10015386.121201

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLKLSHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFFKPKLPRPKHESKPPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMPTSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACTACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCGCTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTGTGTGGAGCTGTGGTCTCTGCCTCCAGTGTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTGTGGAGACTTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAAGTGTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATGTGA
 AAAACAACCTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAAATGGATGTTGGAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

10015335, 121201

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

1015336.121201

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTGCCTCCGCTCAGAAGCTCCGTGGCGCGCGCACCCTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTCTTTTCTTTTCTTCAAGTCTTGATTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTT
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTGGAAGTCAAT
 TGGGGATTGATGTTACTGCACATACTTTTCAACAACCAAGACATCAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCCTTCTGGATGACATTTTGAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGGTTGTAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAAGCAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCTAGGAAC
 TCTAATTCTGTACATAAAAAATTTTAAAGTTATTTGTTGCTTTCAAGGCAAGTCTGTTCAATG
 CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGAATC
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAACGTGTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACATTCCTTCAGAATAACTGA
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTTAATAACAGCATTAAAAATAGTT
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTATGATGAGAGTAACAATA
 AAGTATTCATGATTTTTCACATACATGAATGTTTCAATTTAAAGTTTAACTCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGGAAAGTGTAACTTATATTATATAAGAGTATC
 CTTTATGAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAATAAGAACATTTAAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
 GTATATAGCACAGGGGAACCTTAATCTTGGGTAATCTAGTATAAAACAATATACTTTTAT
 TTAATTTCCCTTGTAGCAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCTATAGTAACCTGTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
 TGTATTGTTGCTCATTAATATGCTACCACATGTAGCAATAATTACAATATTTTATAAAA
 TAAATATGTGAATATTTGTTTCATGAAAGACAGATTTCCAATCTCTCTTCTCTCTCTGTA
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

1001536.121201

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

10015386.121201

FIGURE 231

CGCGGCCGGGCCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCTGTGCTGCTGCTGCGCGTGAGTGGGGCCAGACAACCCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCCTTTTCGACAGCTTCAGCTGACTCGG
 GTGGATTGTAGCGCCTGGGCCCCACATCATGCGGTGCCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAAACCGGCTGGAGATGTTGAATGAGTCGGTGTGGCGGGCCGGGCT
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCTGCCC
 TTCTCCCGCCTTCGTAACCTGGAGTCGCTTGACCTCAGCCACAATGGCCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGCGCGGCCACTACAGTGGACCTCTCC
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCTGCTGCGCCCCACCAT
 TCAGAGCCTGAACCTGGCCCTGGAAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGCCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCGCTGAGCTACCGGCCCTGCAGGTCTTGACCTGTGCGGCAACCCCAAGCTTAAT
 GGGCAGGAGCTGAGGTGTTTTGAGCCTGAGCTCCCTGAGGAGCTGGACCTTCGCGGCCACC
 AACCTGGTGCCCTGCTGAGGCGCTGCTCTCCACCTCCCGGCATCGAGAGCTGACAGCT
 GGGCCAGGATGTGCGGTGCCGGCGCTGGTGGGGAGGGACCTACCCCGGAGGCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCGCAGGGGCCACC
 ATCTTGT**GA**CAAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG
 GTCCCGAGTAACCTTATGTTCAATGTGCCAACACAGTGGGGAGCCCGCAGGCCATGTGTGCA
 GCGTCACCAAGGAGTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCCTCCTGCTTCCCTTCCCACCTTATCCCCAAGTGCCCTTCCCTCAT
 GCCTGGGCGCGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTTCTAACATAGCCCTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCTCATGTGAC
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCAATGCACCTTTCTGTCTCCTCTA
 ATAAGCCCAACCTCCCCGCTGGGCTCCCTTGTGCCCTTGCCCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGGCCTCACAAAGTGGGACTCTGGGCCCTCTGACAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTTGGTT
 CCAGCCTAGCCAGTTTCTCACCCTGGGTGGGTTCGGGCTCCCGAGCATCCAGACTGGCAAACCTTACC
 CATTTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTGAGTCCCCACTGGCCCTGAGCAGCAGC
 CCTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGTCTGCGCCGACCATGTCTATGC
 TCTACCCTCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTCTCTAGTCTTCATTTTA
 TAAAGTTGTTGGCTTTTAAACGGAGTGTCACTTCAACCGGCCTCCCCTACCCTGCTGGC
 CGGGATGGAGACATGTCAATTTGTAAGAGCAGAAAAAGGTTGCAATTTGTAAT
 ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGCTGCGCCACAGACAGCCACAGGGCAGTGAGCTCTGTCTTCCCCACTGCTGATG
 CCATCATCTATCTAACCGTCTTGATTTAATAAACACTATAAAAGGTTTAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

10015386.121201

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGGLTHLSLASLQRLPELAPS
GFRELPGLOQLDLSGNPKNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTTCCCCAGTTCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC
 TCTAGTCTTGCCCTTCAAGCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTCTGAGATACGGGGAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCCTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTTCTC
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGTCTTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTAATAAGATTTTGTAAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTTTTACTTGACATGAAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGCGT
 AGGGGGGTATTTCATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTTGTGTAT
 CTTCCAGCCAGGAATCTACAGGCCAGCATGTATTTCTACAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

10015386.121201

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 .aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLT IKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAAGTACCTAGTGAAGGTTTCAGATGCAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATGCGATTTCTGGTGTACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

101536.121201
 101536.121201

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

10015386-121201

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGCGCTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTATGC
 TTAAGAAGTAAAAATGCGAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTC
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTATTCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCCTGCGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAAACAAAAATTAGCCAGGCATGTTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACTCTAGCCTGGGGGAGAAAGTGAAGTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCATAAAATGAGGTTTTTTGGTAAGA
 AAAAAATTTGTCTTATGTATTGAAGAAGTACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAGCTTCTTTTAAAAAGAATTCTCTAATATGACTTTATGTGAGAA

1201336.12401

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

10015386.121201

FIGURE 239

GTTGATGGCAAACCTTCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCCGCAACACTCCGTCTCACCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAGCTGGCCAGGGTGGT
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAGCTGACCCCAAGCCACCCCTTCACTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCCTCTGCGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTGGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCGGGGGGTGCACGTGGTGTGTTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTT**TAG**GGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTGCGCCTCTCCTCCTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTTCGTGAGG
 ACTGTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGGTTTGAACAAAAAAAAAAAAAAAAAAAA

1001536-121201
 1001536-121201

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWMFIRSYSFMSKTI RLPRLAASPTKEIQVKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDES RKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGACCCCTTCTCTGGGACACT**TATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCTGATTTCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC
 CTTTGACCTGCACAACAATGGCCACACAGTGCACCTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCCAGCTCCACCTGCATGGGGTCAGAAAGGATC
 CCCAGGGGGTCAAGAACACCGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCCATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCTTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGGCTCGCTCACAACTCCCCCT
 TGCTACCAGATGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTTGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTTATTTTCATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCA**TAA**ATTCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAGTCCTTACCCCTCACITTTTATGGCCCTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAGTTGTATATTTTTGATCAATA
 TATTTGGAATTAAGTTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTTFDPDLP
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

10015336-121201

FIGURE 243

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
 GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGG
 ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTC
 CGGATCAGGGAACACTACCAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
 ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
 AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC
 TGCACCCACATGTGTTACCAATTTTTGTACACAACTTGGAGCCCAGGGCACTATCCTAAGC
 TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCAT
 CCTGCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCAGCAGGAG
 GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCCTCCCAACTCCCAGTGGC
 ACAGATGACGACTTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
 GGAAGCCACCACAGAATCAGCAAAATGGAATTCAGTAAAGCTGTTTCAAATTTTTTCAACTAAG
 CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTTGATTATATTATGGAATAGATTGA
 GACACATTGGATAGTCTTAGAAGAAATTAATTCCTTAATTTACCTGAAAATATTCTTGAAAT
 TCAGAAAATATGTTCTATGTAGAGAATCCCACTTTTAAAAACAATAATTCATGGATAAAT
 CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTTAAACATATTTGAAA
 ACTGGAAA
 AAAAAAAAAAAAAAAAAA

101536-12101

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNOVFPSLSLIPLTQM
LTLGPDHLHLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPVFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

1015386.121201

FIGURE 245

GGAGAGAGGCGCGGGGTGAAAGGCGCATTGATGCAGCCTCGCGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCCTCC
 TGCTGCTCTGCTGCTGCAGTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG
 GGATCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG
 GAGTCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAAGACCTCTTCCCATGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAAGATTACCCAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTCACTGTTTTTAAATCTAGCATTATTCAATTTGCTTCAATCAAAGT
 GTTTTCAATATTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTTGTTGTGGTCTTTTGTCTTTCTCTTAGTATAGCATTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT
 AAAAATTATTTCCAACA

10015336.121201
 10015336.121201

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTFGIPGRDGFKEGKECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDDYKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

10015385-121201